

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: BROW, MARY ANN D.
LYAMICHEV, VICTOR I.
OLIVE, DAVID M.
- (ii) TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF PATHOGENS
- (iii) NUMBER OF SEQUENCES: 160
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: MEDLEN & CARROLL
(B) STREET: 220 MONTGOMERY STREET, SUITE 2200
(C) CITY: SAN FRANCISCO
(D) STATE: CALIFORNIA
(E) COUNTRY: UNITED STATES OF AMERICA
(F) ZIP: 94104
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Patent in Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: CARROLL, PETER G.
(B) REGISTRATION NUMBER: 32,837
(C) REFERENCE/DOCKET NUMBER: FORS-01756
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (415) 705-8410
(B) TELEFAX: (415) 397-8338

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2506 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | |
|--|-----|
| ATGAGGGGGA TGCTGCCCCCT CTTTGAGCCC AAGGGCCGGG TCCTCCTGGT GGACGGCCAC | 60 |
| CACCTGGCCT ACCGCACCTT CCACGCCCTG AAGGGCCTCA CCACCAGCCG GGGGGAGCCG | 120 |
| GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTCAAGGA GGACGGGGAC | 180 |
| GCGGTGATCG TGGTCTTTGA CGCCAAGGCC CCCTCCTTCC GCCACGAGGC CTACGGGGGG | 240 |
| TACAAGGCGG GCCGGGCCCC CACGCCGGAG GACTTTCCCC GGCAACTCGC CCTCATCAAG | 300 |

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|------------|------------|------------|------------|------------|------------|------|
| GAGCTGGTGG | ACCTCCTGGG | GCTGGCGCGC | CTCGAGGTCC | CGGGCTACGA | GGCGGACGAC | 360 |
| GTCCTGGCCA | GCCTGGCCAA | GAAGGCGGAA | AAGGAGGGCT | ACGAGGTCCG | CATCCTCACC | 420 |
| GCCGACAAAG | ACCTTTACCA | GCTCCTTTCC | GACCGCATCC | ACGTCCTCCA | CCCCGAGGGG | 480 |
| TACCTCATCA | CCCCGGCCTG | GCTTTGGGAA | AAGTACGGCC | TGAGGCCCCG | CCAGTGGGCC | 540 |
| GACTACCGGG | CCCTGACCGG | GGACGAGTCC | GACAACCTTC | CCGGGGTCAA | GGGCATCGGG | 600 |
| GAGAAGACGG | CGAGGAAGCT | TCTGGAGGAG | TGGGGGAGCC | TGGAAGCCCT | CCTCAAGAAC | 660 |
| CTGGACCGGC | TGAAGCCCGC | CATCCGGGAG | AAGATCCTGG | CCCACATGGA | CGATCTGAAG | 720 |
| CTCTCCTGGG | ACCTGGCCAA | GGTGCGCACC | GACCTGCCCC | TGGAGGTGGA | CTTCGCCAAA | 780 |
| AGGCGGGAGC | CCGACCGGGA | GAGGCTTAGG | GCCTTTCTGG | AGAGGCTTGA | GTTTGGCAGC | 840 |
| CTCCTCCACG | AGTTCGGCCT | TCTGGAAAGC | CCCAAGGCCC | TGGAGGAGGC | CCCCTGGCCC | 900 |
| CCGCCGGAAG | GGGCCTTCGT | GGGCTTTGTG | CTTTCCCGCA | AGGAGCCCAT | GTGGGCCGAT | 960 |
| CTTCTGGCCC | TGGCCGCCGC | CAGGGGGGGC | CGGGTCCACC | GGGCCCCCGA | GCCTTATAAA | 1020 |
| GCCCTCAGGG | ACCTGAAGGA | GGCGCGGGGG | CTTCTCGCCA | AAGACCTGAG | CGTTCTGGCC | 1080 |
| CTGAGGGAAG | GCCTTGGCCT | CCCGCCCCGG | GACGACCCCA | TGCTCCTCGC | CTACCTCCTG | 1140 |
| GACCCTTCCA | ACACCACCCC | CGAGGGGGTG | GCCCCGCGCT | ACGGCGGGGA | GTGGACGGAG | 1200 |
| GAGGCGGGGG | AGCGGGCCGC | CCTTTCCGAG | AGGCTCTTCG | CCAACCTGTG | GGGGAGGCTT | 1260 |
| GAGGGGGAGG | AGAGGCTCCT | TTGGCTTTAC | CGGGAGGTGG | AGAGGCCCCT | TTCCGCTGTC | 1320 |
| CTGGCCCACA | TGGAGGCCAC | GGGGGTGCGC | CTGGACGTGG | CCTATCTCAG | GGCCTTGTC | 1380 |
| CTGGAGGTGG | CCGAGGAGAT | CGCCCGCCTC | GAGGCCGAGG | TCTTCCGCCT | GGCCGGCCAC | 1440 |
| CCCTTCAACC | TCAACTCCCG | GGACCAGCTG | GAAAGGGTCC | TCTTTGACGA | GCTAGGGCTT | 1500 |
| CCCCCCATCG | GCAAGACGGA | GAAGACCGGC | AAGCGCTCCA | CCAGCGCCGC | CGTCCTGGAG | 1560 |
| GCCCTCCGCG | AGGCCACCC | CATCGTGGAG | AAGATCCTGC | AGTACCGGGA | GCTACCAAG | 1620 |
| CTGAAGAGCA | CCTACATTGA | CCCCTTGCCG | GACCTCATCC | ACCCCAGGAC | GGGCCGCCTC | 1680 |
| CACCCCCGCT | TCAACCAGAC | GGCCACGGCC | ACGGGCAGGC | TAAGTAGCTC | CGATCCCAAC | 1740 |
| CTCCAGAACA | TCCCCGTCCG | CACCCCGCTT | GGGCAGAGGA | TCCGCCGGGC | CTTCATCGCC | 1800 |
| GAGGAGGGGT | GGCTATTGGT | GGCCCTGGAC | TATAGCCAGA | TAGAGCTCAG | GGTGCTGGCC | 1860 |
| CACCTCTCCG | GCGACGAGAA | CCTGATCCGG | GTCTTCCAGG | AGGGGCGGGA | CATCCACACG | 1920 |
| GAGACCGCCA | GCTGGATGTT | CGGCGTCCCC | CGGGAGGCCG | TGGACCCCTT | GATGCGCCGG | 1980 |
| GCGGCCAAGA | CCATCAACTT | CGGGGTCTCT | TACGGCATGT | CGGCCACCG | CCTCTCCAG | 2040 |
| GAGCTAGCCA | TCCCTTACGA | GGAGGCCAG | GCCTTCATTG | AGCGCTACTT | TCAGAGCTTC | 2100 |
| CCCAAGGTGC | GGGCCTGGAT | TGAGAAGACC | CTGGAGGAGG | GCAGGAGGCG | GGGGTACGTG | 2160 |

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|--|------|
| GAGACCCTCT TCGGCCGCGG CCGCTACGTG CCAGACCTAG AGGCCCCGGT GAAGAGCGTG | 2220 |
| CGGGAGGCGG CCGAGCGCAT GGCCTTCAAC ATGCCCCGTCC AGGGCACCGC CGCCGACCTC | 2280 |
| ATGAAGCTGG CTATGGTGAA GCTCTTCCCC AGGCTGGAGG AAATGGGGGC CAGGATGCTC | 2340 |
| CTTCAGGTCC ACGACGAGCT GGTCTCTGAG GCCCCAAAAG AGAGGGCGGA GGCCGTGGCC | 2400 |
| CGGCTGGCCA AGGAGGTCAT GGAGGGGGTG TATCCCCTGG CCGTGCCCCCT GGAGGTGGAG | 2460 |
| GTGGGGATAG GGGAGGACTG GCTCTCCGCC AAGGAGTGAT ACCACC | 2506 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | |
|--|------|
| ATGGCGATGC TTCCCTCTT TGAGCCCAA GGCCGCGTGC TCCTGGTGGA CGGCCACCAC | 60 |
| CTGGCCTACC GCACCTTCTT TGCCCTCAAG GGCCTCACCA CCAGCCGCGG CGAACCCGTT | 120 |
| CAGGCGGTCT ACGGCTTCGC CAAAAGCCTC CTCAAGGCCC TGAAGGAGGA CGGGGACGTG | 180 |
| GTGGTGGTGG TCTTTGACGC CAAGGCCCCC TCCTTCCGCC ACGAGGCCTA CGAGGCCTAC | 240 |
| AAGGCGGGCC GGGCCCCCACC CCCGGAGGAC TTTCCCCGGC AGCTGGCCCT CATCAAGGAG | 300 |
| TTGGTGGACC TCCTAGGCCT TGTGCGGCTG GAGGTTCCCG GCTTTGAGGC GGACGACGTG | 360 |
| CTGGCCACCC TGGCCAAGCG GCGGAAAAG GAGGGGTACG AGGTGCGCAT CCTACTGCC | 420 |
| GACCGCGACC TCTACCAGCT CCTTTCCGAG CGCATCGCCA TCCTCCACCC TGAGGGGTAC | 480 |
| CTGATCACCC CGGCGTGGCT TTACGAGAAG TACGGCCTGC GCCCGGAGCA GTGGGTGGAC | 540 |
| TACCGGGCCC TGGCGGGGGA CCCCTCGGAT AACATCCCCG GGGTGAAGGG CATCGGGGAG | 600 |
| AAGACCGCCC AGAGGCTCAT CCGCGAGTGG GGGAGCCTGG AAAACCTCTT CCAGCACCTG | 660 |
| GACCAGGTGA AGCCCTCCTT GCGGGAGAAG CTCCAGGCGG GCATGGAGGC CCTGGCCCTT | 720 |
| TCCCGGAAGC TTTCCAGGT GCACACTGAC CTGCCCCCTG AGGTGGACTT CGGGAGGCGC | 780 |
| CGCACACCCA ACCTGGAGGG TCTGCGGGCT TTTTGGAGC GGTGGAGTT TGGAAGCCTC | 840 |
| CTCCACGAGT TCGGCCTCCT GGAGGGGCCG AAGGCGGCAG AGGAGGCCCC CTGGCCCCCT | 900 |
| CCGGAAGGGG CTTTTTTGGG CTTTTCTTT TCCCGTCCCC AGCCCATGTG GGCCGAGCTT | 960 |
| CTGGCCCTGG CTGGGGCGTG GGAGGGGCGC CTCCATCGGG CACAAGACCC CTTAGGGGC | 1020 |
| CTGAGGGACC TTAAGGGGGT GCGGGGAATC CTGGCCAAGG ACCTGGCGGT TTTGGCCCTG | 1080 |
| CGGGAGGGCC TGGACCTCTT CCCAGAGGAC GACCCCATGC TCCTGGCCTA CCTTCTGGAC | 1140 |

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|---|------|
| CCCTCCAACA CCACCCCTGA GGGGGTGGCC CGGCGTTACG GGGGGGAGTG GACGGAGGAT | 1200 |
| GCGGGGGAGA GGGCCCTCCT GGCCGAGCGC CTCTTCCAGA CCCTAAAGGA GCGCCTTAAG | 1260 |
| GGAGAAGAAC GCCTGCTTTG GCTTTACGAG GAGGTGGAGA AGCCGCTTTC CCGGGTGTG | 1320 |
| GCCCCGATGG AGGCCACGGG GGTCCGGCTG GACGTGGCCT ACCTCCAGGC CCTCTCCCTG | 1380 |
| GAGGTGGAGG CGGAGGTGCG CCAGCTGGAG GAGGAGGTCT TCCGCCTGGC CGGCCACCCC | 1440 |
| TTCAACCTCA ACTCCCGCGA CCAGCTGGAG CGGGTGCTCT TTGACGAGCT GGGCCTGCCT | 1500 |
| GCCATCGGCA AGACGGAGAA GACGGGGAAA CGCTCCACCA GCGCTGCCGT GCTGGAGGCC | 1560 |
| CTGCGAGAGG CCCACCCCAT CGTGGACCGC ATCCTGCAGT ACCGGGAGCT CACCAAGCTC | 1620 |
| AAGAACACCT ACATAGACCC CCTGCCCGCC CTGGTCCACC CCAAGACCGG CCGGCTCCAC | 1680 |
| ACCCGCTTCA ACCAGACGGC CACCGCCACG GGCAGGCTTT CCAGCTCCGA CCCCACCTG | 1740 |
| CAGAACATCC CCGTGCGCAC CCCTCTGGGC CAGCGCATCC GCCGAGCCTT CGTGGCCGAG | 1800 |
| GAGGGCTGGG TGCTGGTGGT CTTGGACTAC AGCCAGATTG AGCTTCGGGT CCTGGCCCAC | 1860 |
| CTCTCCGGGG ACGAGAACCT GATCCGGGTC TTTCAGGAGG GGAGGGACAT CCACACCCAG | 1920 |
| ACCGCCAGCT GGATGTTGCG CGTTTCCCCC GAAGGGGTAG ACCCTCTGAT GCGCCGGGCG | 1980 |
| GCCAAGACCA TCAACTTCGG GTGCTCTAC GGCATGTCCG CCCACCGCCT CTCCGGGGAG | 2040 |
| CTTTCCATCC CCTACGAGGA GGCGGTGGCC TTCATTGAGC GCTACTTCCA GAGCTACCCC | 2100 |
| AAGGTGCGGG CCTGGATTGA GGGGACCCTC GAGGAGGGCC GCCGGCGGGG GTATGTGGAG | 2160 |
| ACCCTCTTCG GCCGCCGGCG CTATGTGCCC GACCTCAACG CCCGGGTGAA GAGCGTGCGE | 2220 |
| GAGGCGGCGG AGCGCATGGC CTTCAACATG CCGGTCCAGG GCACCGCCGC CGACCTCATG | 2280 |
| AAGCTGGCCA TGGTGCGGCT TTTCCCCCGG CTTCAGGAAC TGGGGGCGAG GATGCTTTTG | 2340 |
| CAGGTGCACG ACGAGCTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGAG GGTAGCCGCT | 2400 |
| TTGGCCAAGG AGGTCATGGA GGGGGTCTGG CCCCTGCAGG TGCCCCTGGA GGTGGAGGTG | 2460 |
| GGCCTGGGGG AGGACTGGCT CTCCGCCAAG GAGTAG | 2496 |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | |
|--|-----|
| ATGGAGGCGA TGCTTCCGCT CTTTGAACCC AAAGGCCGGG TCCTCCTGGT GGACGGCCAC | 60 |
| CACCTGGCCT ACCGCACCTT CTTGCCCCCTG AAGGGCCTCA CCACGAGCCG GGGCGAACCG | 120 |

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|---|------|
| GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTGAAGGA GGACGGGTAC | 180 |
| AAGGCCGTCT TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGAG | 240 |
| GCCTACAAGG CGGGGAGGGC CCCGACCCCC GAGGACTTCC CCCGGCAGCT CGCCCTCATC | 300 |
| AAGGAGCTGG TGGACCTCCT GGGGTTTACC CGCCTCGAGG TCCCCGGCTA CGAGGCGGAC | 360 |
| GACGTTCTCG CCACCCTGGC CAAGAAGGCG GAAAAGGAGG GGTACGAGGT GCGCATCCTC | 420 |
| ACCGCCGACC GCGACCTCTA CCAACTCGTC TCCGACCGCG TCGCCGTCCT CCACCCCGAG | 480 |
| GGCCACCTCA TCACCCCGGA GTGGCTTTGG GAGAAGTACG GCCTCAGGCC GGAGCAGTGG | 540 |
| GTGGACTTCC GCGCCCTCGT GGGGGACCCC TCCGACAACC TCCCCGGGGT CAAGGGCATC | 600 |
| GGGAGAAGA CCGCCCTCAA GCTCCTCAAG GAGTGGGGAA GCCTGGAAAA CCTCCTCAAG | 660 |
| AACCTGGACC GGGTAAAGCC AGAAAACGTC CGGGAGAAGA TCAAGGCCCA CCTGGAAGAC | 720 |
| CTCAGGCTCT CTTGGAGCT CTCCCGGGTG CGCACCGACC TCCCCCTGGA GGTGGACCTC | 780 |
| GCCCAGGGGC GGGAGCCCGA CCGGGAGGGG CTTAGGGCCT TCCTGGAGAG GCTGGAGTTC | 840 |
| GGCAGCCTCC TCCACGAGTT CGGCCTCCTG GAGGCCCCCG CCCCCCTGGA GGAGGCCCCC | 900 |
| TGGCCCCCGC CGGAAGGGGC CTTCTGTGGC TTCGTCTCTT CCCGCCCCGA GCCCATGTGG | 960 |
| GCGGAGCTTA AAGCCCTGGC CGCCTGCAGG GACGGCCGGG TGCACCGGGC AGCAGACCCC | 1020 |
| TTGGCGGGGC TAAAGGACCT CAAGGAGGTC CGGGGCCTCC TCGCCAAGGA CCTCGCCGTC | 1080 |
| TTGGCCTCGA GGGAGGGGCT AGACCTCGTG CCCGGGGACG ACCCCATGCT CCTCGCCTAC | 1140 |
| CTCCTGGACC CCTCCAACAC CACCCCGAG GGGGTGGCGC GGCGCTACGG GGGGGAGTGG | 1200 |
| ACGGAGGACG CCGCCCACCG GGCCCTCCTC TCGGAGAGGC TCCATCGGAA CCTCCTTAAG | 1260 |
| CGCCTCGAGG GGGAGGAGAA GCTCCTTTGG CTCTACCACG AGGTGGAAAA GCCCCTCTCC | 1320 |
| CGGGTCTTGG CCCACATGGA GGCCACCGGG GTACGGCTGG ACGTGGCCTA CTTTCAGGCC | 1380 |
| CTTTCCCTGG AGCTTGCGGA GGAGATCCGC CGCCTCGAGG AGGAGGTCTT CCGCTTGGCG | 1440 |
| GGCCACCCCT TCAACCTCAA CTCCCGGGAC CAGCTGGAAA GGGTGCTCTT TGACGAGCTT | 1500 |
| AGGCTTCCCG CTTTGGGGAA GACGCAAAAG ACAGGCAAGC GCTCCACCAG CGCCGCGGTG | 1560 |
| CTGGAGGCCC TACGGGAGGC CCACCCCATC GTGGAGAAGA TCCTCCAGCA CCGGGAGCTC | 1620 |
| ACCAAGCTCA AGAACACCTA CGTGGACCCC CTCCCAAGCC TCGTCCACCC GAGGACGGGC | 1680 |
| CGCCTCCACA CCCGCTTCAA CCAGACGGCC ACGGCCACGG GGAGGCTTAG TAGCTCCGAC | 1740 |
| CCCAACCTGC AGAATATCCC CGTCCGACC CCCTTGGGCC AGAGGATCCG CCGGGCCTTC | 1800 |
| GTGGCCGAGG CGGGTTGGGC GTTGGTGGCC CTGGACTATA GCCAGATAGA GCTCCGCGTC | 1860 |
| CTCGCCACCC TCTCCGGGGA CGAAAACCTG ATCAGGGTCT TCCAGGAGGG GAAGGACATC | 1920 |
| CACACCCAGA CCGCAAGCTG GATGTTCCGC GTCCCCCGG AGGCCGTGGA CCCCCTGATG | 1980 |

CGCCGGGCGG CCAAGACGGT GAACTTCGGC GTCCTCTACG GCATGTCCGC CCATAGGCTC 2040
 TCCCAGGAGC TTGCCATCCC CTACGAGGAG GCGGTGGCCT TTATAGAGGC TACTTCCAAA 2100
 GCTTCCCCAA GGTGCGGGCC TGGATAGAAA AGACCCTGGA GGAGGGGAGG AAGCGGGGCT 2160
 ACGTGGAAAC CCTCTTCGGA AGAAGGCGCT ACGTGCCCGA CCTCAACGCC CGGGTGAAGA 2220
 GCGTCAGGGA GGCCGCGGAG CGCATGGCCT TCAACATGCC CGTCCAGGGC ACCGCCGCCG 2280
 ACCTCATGAA GCTCGCCATG GTGAAGCTCT TCCCCGCCT CCGGGAGATG GGGGCCCGCA 2340
 TGCTCCTCCA GGTCCACGAC GAGCTCCTCC TGGAGGCCCC CCAAGCGCGG GCCGAGGAGG 2400
 TGGCGGCTTT GGCCAAGGAG GCCATGGAGA AGGCCTATCC CCTCGCCGTG CCCCTGGAGG 2460
 TGGAGGTGGG GATGGGGGAG GACTGGCTTT CCGCCAAGGG TTAG 2504

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
 1 5 10 15
 Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly
 20 25 30
 Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
 35 40 45
 Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val
 50 55 60
 Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly
 65 70 75 80
 Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
 85 90 95
 Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu
 100 105 110
 Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys
 115 120 125
 Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp
 130 135 140
 Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly
 145 150 155 160
 Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
 165 170 175

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Asp | Gln | Trp | Ala | Asp | Tyr | Arg | Ala | Leu | Thr | Gly | Asp | Glu | Ser | Asp | Asn | | |
| | | | 180 | | | | | | 185 | | | | | 190 | | | |
| Leu | Pro | Gly | Val | Lys | Gly | Ile | Gly | Glu | Lys | Thr | Ala | Arg | Lys | Leu | Leu | | |
| | | 195 | | | | | 200 | | | | | 205 | | | | | |
| Glu | Glu | Trp | Gly | Ser | Leu | Glu | Ala | Leu | Leu | Lys | Asn | Leu | Asp | Arg | Leu | | |
| | | 210 | | | | 215 | | | | | 220 | | | | | | |
| Lys | Pro | Ala | Ile | Arg | Glu | Lys | Ile | Leu | Ala | His | Met | Asp | Asp | Leu | Lys | | |
| | 225 | | | | 230 | | | | | 235 | | | | | 240 | | |
| Leu | Ser | Trp | Asp | Leu | Ala | Lys | Val | Arg | Thr | Asp | Leu | Pro | Leu | Glu | Val | | |
| | | | 245 | | | | | 250 | | | | | | 255 | | | |
| Asp | Phe | Ala | Lys | Arg | Arg | Glu | Pro | Asp | Arg | Glu | Arg | Leu | Arg | Ala | Phe | | |
| | | 260 | | | | | | 265 | | | | | | 270 | | | |
| Leu | Glu | Arg | Leu | Glu | Phe | Gly | Ser | Leu | Leu | His | Glu | Phe | Gly | Leu | Leu | | |
| | | 275 | | | | | 280 | | | | | 285 | | | | | |
| Glu | Ser | Pro | Lys | Ala | Leu | Glu | Glu | Ala | Pro | Trp | Pro | Pro | Pro | Glu | Gly | | |
| | 290 | | | | | 295 | | | | | 300 | | | | | | |
| Ala | Phe | Val | Gly | Phe | Val | Leu | Ser | Arg | Lys | Glu | Pro | Met | Trp | Ala | Asp | | |
| | 305 | | | | 310 | | | | | 315 | | | | | 320 | | |
| Leu | Leu | Ala | Leu | Ala | Ala | Ala | Arg | Gly | Gly | Arg | Val | His | Arg | Ala | Pro | | |
| | | | 325 | | | | | | 330 | | | | | 335 | | | |
| Glu | Pro | Tyr | Lys | Ala | Leu | Arg | Asp | Leu | Lys | Glu | Ala | Arg | Gly | Leu | Leu | | |
| | | | 340 | | | | | 345 | | | | | 350 | | | | |
| Ala | Lys | Asp | Leu | Ser | Val | Leu | Ala | Leu | Arg | Glu | Gly | Leu | Gly | Leu | Pro | | |
| | | 355 | | | | | 360 | | | | | 365 | | | | | |
| Pro | Gly | Asp | Asp | Pro | Met | Leu | Leu | Ala | Tyr | Leu | Leu | Asp | Pro | Ser | Asn | | |
| | 370 | | | | | 375 | | | | | 380 | | | | | | |
| Thr | Thr | Pro | Glu | Gly | Val | Ala | Arg | Arg | Tyr | Gly | Gly | Glu | Trp | Thr | Glu | | |
| | 385 | | | | 390 | | | | | 395 | | | | | 400 | | |
| Glu | Ala | Gly | Glu | Arg | Ala | Ala | Leu | Ser | Glu | Arg | Leu | Phe | Ala | Asn | Leu | | |
| | | | 405 | | | | | | 410 | | | | | 415 | | | |
| Trp | Gly | Arg | Leu | Glu | Gly | Glu | Glu | Arg | Leu | Leu | Trp | Leu | Tyr | Arg | Glu | | |
| | | | 420 | | | | | 425 | | | | | 430 | | | | |
| Val | Glu | Arg | Pro | Leu | Ser | Ala | Val | Leu | Ala | His | Met | Glu | Ala | Thr | Gly | | |
| | | 435 | | | | | 440 | | | | | 445 | | | | | |
| Val | Arg | Leu | Asp | Val | Ala | Tyr | Leu | Arg | Ala | Leu | Ser | Leu | Glu | Val | Ala | | |
| | 450 | | | | | 455 | | | | | 460 | | | | | | |
| Glu | Glu | Ile | Ala | Arg | Leu | Glu | Ala | Glu | Val | Phe | Arg | Leu | Ala | Gly | His | | |
| | 465 | | | | 470 | | | | | 475 | | | | 480 | | | |
| Pro | Phe | Asn | Leu | Asn | Ser | Arg | Asp | Gln | Leu | Glu | Arg | Val | Leu | Phe | Asp | | |
| | | | 485 | | | | | 490 | | | | | | 495 | | | |
| Glu | Leu | Gly | Leu | Pro | Ala | Ile | Gly | Lys | Thr | Glu | Lys | Thr | Gly | Lys | Arg | | |
| | | 500 | | | | | | 505 | | | | | 510 | | | | |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Thr | Ser | Ala | Ala | Val | Leu | Glu | Ala | Leu | Arg | Glu | Ala | His | Pro | Ile |
| | | 515 | | | | | 520 | | | | | 525 | | | |
| Val | Glu | Lys | Ile | Leu | Gln | Tyr | Arg | Glu | Leu | Thr | Lys | Leu | Lys | Ser | Thr |
| | 530 | | | | | 535 | | | | | 540 | | | | |
| Tyr | Ile | Asp | Pro | Leu | Pro | Asp | Leu | Ile | His | Pro | Arg | Thr | Gly | Arg | Leu |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 |
| His | Thr | Arg | Phe | Asn | Gln | Thr | Ala | Thr | Ala | Thr | Gly | Arg | Leu | Ser | Ser |
| | | | | 565 | | | | | 570 | | | | | 575 | |
| Ser | Asp | Pro | Asn | Leu | Gln | Asn | Ile | Pro | Val | Arg | Thr | Pro | Leu | Gly | Gln |
| | | | 580 | | | | | 585 | | | | | 590 | | |
| Arg | Ile | Arg | Arg | Ala | Phe | Ile | Ala | Glu | Glu | Gly | Trp | Leu | Leu | Val | Ala |
| | | 595 | | | | | 600 | | | | | 605 | | | |
| Leu | Asp | Tyr | Ser | Gln | Ile | Glu | Leu | Arg | Val | Leu | Ala | His | Leu | Ser | Gly |
| | 610 | | | | | 615 | | | | | 620 | | | | |
| Asp | Glu | Asn | Leu | Ile | Arg | Val | Phe | Gln | Glu | Gly | Arg | Asp | Ile | His | Thr |
| 625 | | | | | 630 | | | | | 635 | | | | | 640 |
| Glu | Thr | Ala | Ser | Trp | Met | Phe | Gly | Val | Pro | Arg | Glu | Ala | Val | Asp | Pro |
| | | | | 645 | | | | | 650 | | | | | 655 | |
| Leu | Met | Arg | Arg | Ala | Ala | Lys | Thr | Ile | Asn | Phe | Gly | Val | Leu | Tyr | Gly |
| | | | 660 | | | | | 665 | | | | | 670 | | |
| Met | Ser | Ala | His | Arg | Leu | Ser | Gln | Glu | Leu | Ala | Ile | Pro | Tyr | Glu | Glu |
| | | 675 | | | | | 680 | | | | | 685 | | | |
| Ala | Gln | Ala | Phe | Ile | Glu | Arg | Tyr | Phe | Gln | Ser | Phe | Pro | Lys | Val | Arg |
| | 690 | | | | | 695 | | | | | 700 | | | | |
| Ala | Trp | Ile | Glu | Lys | Thr | Leu | Glu | Glu | Gly | Arg | Arg | Arg | Gly | Tyr | Val |
| 705 | | | | | 710 | | | | | 715 | | | | | 720 |
| Glu | Thr | Leu | Phe | Gly | Arg | Arg | Arg | Tyr | Val | Pro | Asp | Leu | Glu | Ala | Arg |
| | | | | 725 | | | | | 730 | | | | | 735 | |
| Val | Lys | Ser | Val | Arg | Glu | Ala | Ala | Glu | Arg | Met | Ala | Phe | Asn | Met | Pro |
| | | | 740 | | | | | 745 | | | | | 750 | | |
| Val | Gln | Gly | Thr | Ala | Ala | Asp | Leu | Met | Lys | Leu | Ala | Met | Val | Lys | Leu |
| | | 755 | | | | | 760 | | | | | 765 | | | |
| Phe | Pro | Arg | Leu | Glu | Glu | Met | Gly | Ala | Arg | Met | Leu | Leu | Gln | Val | His |
| | 770 | | | | | 775 | | | | | 780 | | | | |
| Asp | Glu | Leu | Val | Leu | Glu | Ala | Pro | Lys | Glu | Arg | Ala | Glu | Ala | Val | Ala |
| 785 | | | | | 790 | | | | | 795 | | | | | 800 |
| Arg | Leu | Ala | Lys | Glu | Val | Met | Glu | Gly | Val | Tyr | Pro | Leu | Ala | Val | Pro |
| | | | | 805 | | | | | 810 | | | | | 815 | |
| Leu | Glu | Val | Glu | Val | Gly | Ile | Gly | Glu | Asp | Trp | Leu | Ser | Ala | Lys | Glu |
| | | | 820 | | | | | 825 | | | | | 830 | | |

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 831 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Met | Leu | Pro | Leu | Phe | Glu | Pro | Lys | Gly | Arg | Val | Leu | Leu | Val | 1 | 5 | 10 | 15 |
| Asp | Gly | His | His | Leu | Ala | Tyr | Arg | Thr | Phe | Phe | Ala | Leu | Lys | Gly | Leu | 20 | 25 | 30 | |
| Thr | Thr | Ser | Arg | Gly | Glu | Pro | Val | Gln | Ala | Val | Tyr | Gly | Phe | Ala | Lys | 35 | 40 | 45 | |
| Ser | Leu | Leu | Lys | Ala | Leu | Lys | Glu | Asp | Gly | Asp | Val | Val | Val | Val | Val | 50 | 55 | 60 | |
| Phe | Asp | Ala | Lys | Ala | Pro | Ser | Phe | Arg | His | Glu | Ala | Tyr | Glu | Ala | Tyr | 65 | 70 | 75 | 80 |
| Lys | Ala | Gly | Arg | Ala | Pro | Thr | Pro | Glu | Asp | Phe | Pro | Arg | Gln | Leu | Ala | 85 | 90 | 95 | |
| Leu | Ile | Lys | Glu | Leu | Val | Asp | Leu | Leu | Gly | Leu | Val | Arg | Leu | Glu | Val | 100 | 105 | 110 | |
| Pro | Gly | Phe | Glu | Ala | Asp | Asp | Val | Leu | Ala | Thr | Leu | Ala | Lys | Arg | Ala | 115 | 120 | 125 | |
| Glu | Lys | Glu | Gly | Tyr | Glu | Val | Arg | Ile | Leu | Thr | Ala | Asp | Arg | Asp | Leu | 130 | 135 | 140 | |
| Tyr | Gln | Leu | Leu | Ser | Glu | Arg | Ile | Ala | Ile | Leu | His | Pro | Glu | Gly | Tyr | 145 | 150 | 155 | 160 |
| Leu | Ile | Thr | Pro | Ala | Trp | Leu | Tyr | Glu | Lys | Tyr | Gly | Leu | Arg | Pro | Glu | 165 | 170 | 175 | |
| Gln | Trp | Val | Asp | Tyr | Arg | Ala | Leu | Ala | Gly | Asp | Pro | Ser | Asp | Asn | Ile | 180 | 185 | 190 | |
| Pro | Gly | Val | Lys | Gly | Ile | Gly | Glu | Lys | Thr | Ala | Gln | Arg | Leu | Ile | Arg | 195 | 200 | 205 | |
| Glu | Trp | Gly | Ser | Leu | Glu | Asn | Leu | Phe | Gln | His | Leu | Asp | Gln | Val | Lys | 210 | 215 | 220 | |
| Pro | Ser | Leu | Arg | Glu | Lys | Leu | Gln | Ala | Gly | Met | Glu | Ala | Leu | Ala | Leu | 225 | 230 | 235 | 240 |
| Ser | Arg | Lys | Leu | Ser | Gln | Val | His | Thr | Asp | Leu | Pro | Leu | Glu | Val | Asp | 245 | 250 | 255 | |
| Phe | Gly | Arg | Arg | Arg | Thr | Pro | Asn | Leu | Glu | Gly | Leu | Arg | Ala | Phe | Leu | 260 | 265 | 270 | |
| Glu | Arg | Leu | Glu | Phe | Gly | Ser | Leu | Leu | His | Glu | Phe | Gly | Leu | Leu | Glu | | | | |

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| 275 | | | | | 280 | | | | | 285 | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Pro | Lys | Ala | Ala | Glu | Glu | Ala | Pro | Trp | Pro | Pro | Pro | Glu | Gly | Ala |
| 290 | | | | | 295 | | | | | 300 | | | | | |
| Phe | Leu | Gly | Phe | Ser | Phe | Ser | Arg | Pro | Glu | Pro | Met | Trp | Ala | Glu | Leu |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Leu | Ala | Leu | Ala | Gly | Ala | Trp | Glu | Gly | Arg | Leu | His | Arg | Ala | Gln | Asp |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Pro | Leu | Arg | Gly | Leu | Arg | Asp | Leu | Lys | Gly | Val | Arg | Gly | Ile | Leu | Ala |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Lys | Asp | Leu | Ala | Val | Leu | Ala | Leu | Arg | Glu | Gly | Leu | Asp | Leu | Phe | Pro |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Glu | Asp | Asp | Pro | Met | Leu | Leu | Ala | Tyr | Leu | Leu | Asp | Pro | Ser | Asn | Thr |
| | 370 | | | | | | 375 | | | | 380 | | | | |
| Thr | Pro | Glu | Gly | Val | Ala | Arg | Arg | Tyr | Gly | Gly | Glu | Trp | Thr | Glu | Asp |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Ala | Gly | Glu | Arg | Ala | Leu | Leu | Ala | Glu | Arg | Leu | Phe | Gln | Thr | Leu | Lys |
| | | | | 405 | | | | | 410 | | | | | 415 | |
| Glu | Arg | Leu | Lys | Gly | Glu | Glu | Arg | Leu | Leu | Trp | Leu | Tyr | Glu | Glu | Val |
| | | | 420 | | | | | 425 | | | | | 430 | | |
| Glu | Lys | Pro | Leu | Ser | Arg | Val | Leu | Ala | Arg | Met | Glu | Ala | Thr | Gly | Val |
| | | 435 | | | | | 440 | | | | | 445 | | | |
| Arg | Leu | Asp | Val | Ala | Tyr | Leu | Gln | Ala | Leu | Ser | Leu | Glu | Val | Glu | Ala |
| | 450 | | | | | 455 | | | | | 460 | | | | |
| Glu | Val | Arg | Gln | Leu | Glu | Glu | Glu | Val | Phe | Arg | Leu | Ala | Gly | His | Pro |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 |
| Phe | Asn | Leu | Asn | Ser | Arg | Asp | Gln | Leu | Glu | Arg | Val | Leu | Phe | Asp | Glu |
| | | | | 485 | | | | | 490 | | | | | 495 | |
| Leu | Gly | Leu | Pro | Ala | Ile | Gly | Lys | Thr | Glu | Lys | Thr | Gly | Lys | Arg | Ser |
| | | | 500 | | | | | 505 | | | | | 510 | | |
| Thr | Ser | Ala | Ala | Val | Leu | Glu | Ala | Leu | Arg | Glu | Ala | His | Pro | Ile | Val |
| | | 515 | | | | | 520 | | | | | 525 | | | |
| Asp | Arg | Ile | Leu | Gln | Tyr | Arg | Glu | Leu | Thr | Lys | Leu | Lys | Asn | Thr | Tyr |
| | 530 | | | | | 535 | | | | | 540 | | | | |
| Ile | Asp | Pro | Leu | Pro | Ala | Leu | Val | His | Pro | Lys | Thr | Gly | Arg | Leu | His |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 |
| Thr | Arg | Phe | Asn | Gln | Thr | Ala | Thr | Ala | Thr | Gly | Arg | Leu | Ser | Ser | Ser |
| | | | | 565 | | | | | 570 | | | | | 575 | |
| Asp | Pro | Asn | Leu | Gln | Asn | Ile | Pro | Val | Arg | Thr | Pro | Leu | Gly | Gln | Arg |
| | | | 580 | | | | | 585 | | | | | 590 | | |
| Ile | Arg | Arg | Ala | Phe | Val | Ala | Glu | Glu | Gly | Trp | Val | Leu | Val | Val | Leu |
| | | 595 | | | | | 600 | | | | | 605 | | | |

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| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Tyr | Ser | Gln | Ile | Glu | Leu | Arg | Val | Leu | Ala | His | Leu | Ser | Gly | Asp |
| 610 | | | | | | 615 | | | | | 620 | | | | |
| Glu | Asn | Leu | Ile | Arg | Val | Phe | Gln | Glu | Gly | Arg | Asp | Ile | His | Thr | Gln |
| 625 | | | | | 630 | | | | | 635 | | | | | 640 |
| Thr | Ala | Ser | Trp | Met | Phe | Gly | Val | Ser | Pro | Glu | Gly | Val | Asp | Pro | Leu |
| | | | | 645 | | | | | 650 | | | | | 655 | |
| Met | Arg | Arg | Ala | Ala | Lys | Thr | Ile | Asn | Phe | Gly | Val | Leu | Tyr | Gly | Met |
| | | | 660 | | | | | 665 | | | | | 670 | | |
| Ser | Ala | His | Arg | Leu | Ser | Gly | Glu | Leu | Ser | Ile | Pro | Tyr | Glu | Glu | Ala |
| | | 675 | | | | | 680 | | | | | 685 | | | |
| Val | Ala | Phe | Ile | Glu | Arg | Tyr | Phe | Gln | Ser | Tyr | Pro | Lys | Val | Arg | Ala |
| | 690 | | | | | 695 | | | | | 700 | | | | |
| Trp | Ile | Glu | Gly | Thr | Leu | Glu | Glu | Gly | Arg | Arg | Arg | Gly | Tyr | Val | Glu |
| 705 | | | | | 710 | | | | | 715 | | | | | 720 |
| Thr | Leu | Phe | Gly | Arg | Arg | Arg | Tyr | Val | Pro | Asp | Leu | Asn | Ala | Arg | Val |
| | | | | 725 | | | | | 730 | | | | | 735 | |
| Lys | Ser | Val | Arg | Glu | Ala | Ala | Glu | Arg | Met | Ala | Phe | Asn | Met | Pro | Val |
| | | | 740 | | | | | 745 | | | | | 750 | | |
| Gln | Gly | Thr | Ala | Ala | Asp | Leu | Met | Lys | Leu | Ala | Met | Val | Arg | Leu | Phe |
| | | 755 | | | | | 760 | | | | | 765 | | | |
| Pro | Arg | Leu | Gln | Glu | Leu | Gly | Ala | Arg | Met | Leu | Leu | Gln | Val | His | Asp |
| | 770 | | | | | 775 | | | | | 780 | | | | |
| Glu | Leu | Val | Leu | Glu | Ala | Pro | Lys | Asp | Arg | Ala | Glu | Arg | Val | Ala | Ala |
| 785 | | | | | 790 | | | | | 795 | | | | | 800 |
| Leu | Ala | Lys | Glu | Val | Met | Glu | Gly | Val | Trp | Pro | Leu | Gln | Val | Pro | Leu |
| | | | 805 | | | | | | 810 | | | | | 815 | |
| Glu | Val | Glu | Val | Gly | Leu | Gly | Glu | Asp | Trp | Leu | Ser | Ala | Lys | Glu | |
| | | | 820 | | | | | 825 | | | | | 830 | | |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ala | Met | Leu | Pro | Leu | Phe | Glu | Pro | Lys | Gly | Arg | Val | Leu | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Asp | Gly | His | His | Leu | Ala | Tyr | Arg | Thr | Phe | Phe | Ala | Leu | Lys | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Thr | Thr | Ser | Arg | Gly | Glu | Pro | Val | Gln | Ala | Val | Tyr | Gly | Phe | Ala |
| | | | 35 | | | | 40 | | | | | 45 | | | |

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Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala Val Phe
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
65 70 75 80

Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg
130 135 140

Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His Pro Glu
145 150 155 160

Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175

Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu
195 200 205

Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg
210 215 220

Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu Glu Asp
225 230 235 240

Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu
245 250 255

Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Arg
260 265 270

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
275 280 285

Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro Pro
290 295 300

Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp
305 310 315 320

Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Asp Gly Arg Val His Arg
325 330 335

Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
340 345 350

Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
355 360 365

Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
370 375 380

Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
 755 760 765
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
 770 775 780
 Val His Asp Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
 785 790 795 800
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
 805 810 815
 Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
 820 825 830

Lys Gly

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | |
|--|-----|
| ATGNNGGCGA TGCTTCCCCT CTTTGAGCCC AAAGGCCGGG TCCTCCTGGT GGACGGCCAC | 60 |
| CACCTGGCCT ACCGCACCTT CTTCGCCCTG AAGGGCCTCA CCACCAGCCG GGGCGAACCG | 120 |
| GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTGAAGGA GGACGGGGAC | 180 |
| NNGGCGGTGN TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGAG | 240 |
| GCCTACAAGG CGGGCCGGGC CCCCACCCCG GAGGACTTTC CCCGGCAGCT CGCCCTCATC | 300 |
| AAGGAGCTGG TGGACCTCCT GGGGCTTGCG CGCCTCGAGG TCCCCGGCTA CGAGGCGGAC | 360 |
| GACGTNCTGG CCACCCTGGC CAAGAAGGCG GAAAAGGAGG GGTACGAGGT GCGCATCCTC | 420 |
| ACCGCCGACC GCGACCTCTA CCAGCTCCTT TCCGACCGCA TCGCCGTCCT CCACCCCGAG | 480 |
| GGGTACCTCA TCACCCCGGC GTGGCTTTGG GAGAAGTACG GCCTGAGGCC GGAGCAGTGG | 540 |
| GTGGACTACC GGGCCCTGGC GGGGGACCCC TCCGACAACC TCCCCGGGGT CAAGGGCATC | 600 |
| GGGGAGAAGA CCGCCNGAA GCTCCTCNAG GAGTGGGGGA GCCTGGAAAA CCTCCTCAAG | 660 |
| AACCTGGACC GGGTGAAGCC CGCCNTCCGG GAGAAGATCC AGGCCACAT GGANGACCTG | 720 |
| ANGCTCTCCT GGGAGCTNTC CCAGGTGCGC ACCGACCTGC CCCTGGAGGT GGA CTTCGCC | 780 |
| AAGNGGCGGG AGCCCGACCG GGAGGGGCTT AGGGCCTTTC TGGAGAGGCT GGAGTTTGGC | 840 |

| | |
|--|------|
| AGCCTCCTCC ACGAGTTCGG CCTCCTGGAG GGCCCCAAGG CCCTGGAGGA GGCCCCCTGG | 900 |
| CCCCCGCCGG AAGGGGCCTT CGTGGGCTTT GTCCTTTCCC GCCCGAGCC CATGTGGGCC | 960 |
| GAGCTTCTGG CCCTGGCCGC CGCCAGGGAG GGCCGGGTCC ACCGGGCACC AGACCCCTTT | 1020 |
| ANGGGCCTNA GGGACCTNAA GGAGGTGCGG GGNCTCCTCG CCAAGGACCT GGCCGTTTTG | 1080 |
| GCCCTGAGGG AGGGCCTNGA CCTCNTGCCC GGGGACGACC CCATGCTCCT CGCCTACCTC | 1140 |
| CTGGACCCCT CCAACACCAC CCCCAGGGG GTGGCCCGGC GCTACGGGGG GGAGTGGACG | 1200 |
| GAGGANGCGG GGGAGCGGGC CCTCCTNTCC GAGAGGCTCT TCCNGAACCT NNNGCAGCGC | 1260 |
| CTTGAGGGGG AGGAGAGGCT CTTTTGGCTT TACCAGGAGG TGGAGAAGCC CTTTTCCCGG | 1320 |
| GTCCTGGCCC ACATGGAGGC CACGGGGGTN CGGCTGGACG TGGCCTACCT CCAGGCCCTN | 1380 |
| TCCCTGGAGG TGGCGGAGGA GATCCGCCGC CTCGAGGAGG AGGTCTTCCG CCTGGCCGGC | 1440 |
| CACCCCTTCA ACCTCAACTC CCGGGACCAG CTGGAAAGGG TGCTCTTTGA CGAGCTNGGG | 1500 |
| CTTCCCGCCA TCGGCAAGAC GGAGAAGACN GGCAAGCGCT CCACCAGCGC CGCCGTGCTG | 1560 |
| GAGGCCCTNC GNGAGGCCCA CCCCATCGTG GAGAAGATCC TGCAGTACCG GGAGCTCACC | 1620 |
| AAGCTCAAGA ACACCTACAT NGACCCCTG CCNGNCCTCG TCCACCCAG GACGGGCCGC | 1680 |
| CTCCACACCC GCTTCAACCA GACGGCCACG GCCACGGGCA GGCTTAGTAG CTCCGACCCC | 1740 |
| AACCTGCAGA ACATCCCCGT CCGCACCCCN CTGGGCCAGA GGATCCGCCG GGCCTTCGTG | 1800 |
| GCCGAGGAGG GNTGGGTGTT GGTGGCCCTG GACTATAGCC AGATAGAGCT CCGGGTCCTG | 1860 |
| GCCCACCTCT CCGGGGACGA GAACCTGATC CGGGTCTTCC AGGAGGGGAG GGACATCCA | 1920 |
| ACCCAGACCG CCAGCTGGAT GTTCGGCGTC CCCCCGGAGG CCGTGGACCC CCTGATGCGC | 1980 |
| CGGGCGGCCA AGACCATCAA CTTCGGGGTC CTCTACGGCA TGTCCGCCCA CCGCCTCTCC | 2040 |
| CAGGAGCTTG CCATCCCCTA CGAGGAGGCG GTGGCCTTCA TTGAGCGCTA CTTCAGAGC | 2100 |
| TTCCCCAAGG TGCGGGCCTG GATTGAGAAG ACCCTGGAGG AGGGCAGGAG GCGGGGGTAC | 2160 |
| GTGGAGACCC TCTTCGGCCG CCGGCGCTAC GTGCCCGACC TCAACGCCCG GGTGAAGAGC | 2220 |
| GTGCGGGAGG CGGCGGAGCG CATGGCCTTC AACATGCCCG TCCAGGGCAC CGCCGCCGAC | 2280 |
| CTCATGAAGC TGGCCATGGT GAAGCTCTTC CCCC GGCTNC AGGAAATGGG GGCCAGGATG | 2340 |
| CTCCTNCAGG TCCACGACGA GCTGGTCCTC GAGGCCCCCA AAGAGCGGGC GGAGGNNGTG | 2400 |
| GCCGCTTTGG CCAAGGAGGT CATGGAGGGG GTCTATCCCC TGGCCGTGCC CCTGGAGGTG | 2460 |
| GAGGTGGGGA TGGGGGAGGA CTGGCTCTCC GCCAAGGAGT AG | 2502 |

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 833 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Xaa Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
1 5 10 15
Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly
20 25 30
Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
35 40 45
Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Xaa Val
50 55 60
Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala
65 70 75 80
Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
85 90 95
Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Xaa Arg Leu Glu
100 105 110
Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys
115 120 125
Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp
130 135 140
Leu Tyr Gln Leu Leu Ser Asp Arg Ile Ala Val Leu His Pro Glu Gly
145 150 155 160
Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
165 170 175
Glu Gln Trp Val Asp Tyr Arg Ala Leu Xaa Gly Asp Pro Ser Asp Asn
180 185 190
Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Xaa Lys Leu Leu
195 200 205
Xaa Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg Val
210 215 220
Lys Pro Xaa Xaa Arg Glu Lys Ile Xaa Ala His Met Glu Asp Leu Xaa
225 230 235 240
Leu Ser Xaa Xaa Leu Ser Xaa Val Arg Thr Asp Leu Pro Leu Glu Val
245 250 255
Asp Phe Ala Xaa Arg Arg Glu Pro Asp Arg Glu Gly Leu Arg Ala Phe
260 265 270
Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
275 280 285
Glu Xaa Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
290 295 300

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Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
305 310 315 320

Leu Leu Ala Leu Ala Ala Ala Arg Xaa Gly Arg Val His Arg Ala Xaa
325 330 335

Asp Pro Leu Xaa Gly Leu Arg Asp Leu Lys Glu Val Arg Gly Leu Leu
340 345 350

Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Xaa
355 360 365

Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
370 375 380

Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
385 390 395 400

Asp Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Phe Xaa Asn Leu
405 410 415

Xaa Xaa Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Xaa Glu
420 425 430

Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
435 440 445

Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Val Ala
450 455 460

Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His
465 470 475 480

Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
485 490 495

Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg
500 505 510

Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
515 520 525

Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr
530 535 540

Tyr Ile Asp Pro Leu Pro Xaa Leu Val His Pro Arg Thr Gly Arg Leu
545 550 555 560

His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
565 570 575

Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
580 585 590

Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Xaa Leu Val Ala
595 600 605

Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
610 615 620

Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr
625 630 635 640

Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro
645 650 655

Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
660 665 670

Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
675 680 685

Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
690 695 700

Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val
705 710 715 720

Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg
725 730 735

Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
740 745 750

Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
755 760 765

Phe Pro Arg Leu Xaa Glu Met Gly Ala Arg Met Leu Leu Gln Val His
770 775 780

Asp Glu Leu Val Leu Glu Ala Pro Lys Xaa Arg Ala Glu Xaa Val Ala
785 790 795 800

Ala Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro
805 810 815

Leu Glu Val Glu Val Gly Xaa Gly Glu Asp Trp Leu Ser Ala Lys Glu
820 825 830

Xaa

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1647 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

| | |
|---|-----|
| ATGAATTCGG GGATGCTGCC CCTCTTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC | 60 |
| CACCACCTGG CCTACCGCAC CTTCACGCC CTGAAGGGCC TCACCACCAG CCGGGGGGAG | 120 |
| CCGGTGCAGG CGGTCTACGG CTTCGCCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG | 180 |
| GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG | 240 |
| GGGTACAAGG CGGGCCGGGC CCCCACGCC GAGGACTTTC CCCGGCAACT CGCCCTCATC | 300 |
| AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCGGGCTA CGAGGCGGAC | 360 |

| | |
|---|------|
| GACGTCCTGG CCAGCCTGGC CAAGAAGGCG GAAAAGGAGG GCTACGAGGT CCGCATCCTC | 420 |
| ACCGCCGACA AAGACCTTTA CCAGCTCCTT TCCGACCGCA TCCACGTCCT CCACCCCGAG | 480 |
| GGGTACCTCA TCACCCCGGC CTGGCTTTGG GAAAAGTACG GCCTGAGGCC CGACCACTGG | 540 |
| GCCGACTACC GGGCCCTGAC CGGGGACGAG TCCGACAACC TTCCCGGGGT CAAGGGCATC | 600 |
| GGGGAGAAGA CGGCGAGGAA GCTTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG | 660 |
| AACCTGGACC GGCTGAAGCC CGCCATCCGG GAGAAGATCC TGGCCCACAT GGACGATCTG | 720 |
| AAGCTCTCCT GGGACCTGGC CAAGGTGCGC ACCGACCTGC CCCTGGAGGT GGACTTCGCC | 780 |
| AAAAGGCGGG AGCCCGACCG GGAGAGGCTT AGGGCCTTTC TGGAGAGGCT TGAGTTTGGC | 840 |
| AGCCTCCTCC ACGAGTTCGG CCTTCTGGAA AGCCCCAAGG CCCTGGAGGA GGCCCCCTGG | 900 |
| CCCCCGCCGG AAGGGGCCTT CGTGGGCTTT GTGCTTTCCC GCAAGGAGCC CATGTGGGCC | 960 |
| GATCTTCTGG CCCTGGCCGC CGCCAGGGGG GGCCGGGTCC ACCGGGCCCC CGAGCCTTAT | 1020 |
| AAAGCCCTCA GGGACCTGAA GGAGGCGCGG GGGCTTCTCG CCAAAGACCT GAGCGTTCTG | 1080 |
| GCCCTGAGGG AAGGCCTTGG CCTCCCGCCC GGCACGACC CCATGCTCCT CGCCTACCTC | 1140 |
| CTGGACCCTT CCAACACCAC CCCCAGGGGG GTGGCCCGGC GCTACGGCGG GGAGTGGACG | 1200 |
| GAGGAGGCGG GGGAGCGGGC CGCCCTTTCC GAGAGGCTCT TCGCCAACCT GTGGGGGAGG | 1260 |
| CTTGAGGGGG AGGAGAGGCT CCTTTGGCTT TACCGGGAGG TGGAGAGGCC CCTTTCCGCT | 1320 |
| GTCCTGGCCC ACATGGAGGC CACGGGGGTG CGCCTGGACG TGGCCTATCT CAGGGCCTTG | 1380 |
| TCCCTGGAGG TGGCCGGGGA GATCGCCCGC CTCGAGGCCG AGGTCTTCCG CCTGGCCGGE | 1440 |
| CACCCCTTCA ACCTCAACTC CCGGGACCAG CTGGAAAGGG TCCTCTTTGA CGAGCTAGGG | 1500 |
| CTTCCCGCCA TCGGCAAGAC GGAGAAGACC GGCAAGCGCT CCACCAGCGC CGCCGTCCTG | 1560 |
| GAGGCCCTCC GCGAGGCCCA CCCCATCGTG GAGAAGATCC TGCAGGCATG CAAGCTTGGC | 1620 |
| ACTGGCCGTC GTTTTACAAC GTCGTGA | 1647 |

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2088 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

| | |
|--|-----|
| ATGAATTTCG GGATGCTGCC CCTCTTTGAG CCAAGGGCC GGGTCCTCCT GGTGGACGGC | 60 |
| CACCACCTGG CCTACCGCAC CTTCACGCC CTGAAGGGCC TCACCACCAG CCGGGGGGAG | 120 |
| CCGGTGCAGG CGGTCTACGG CTTCCGAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG | 180 |

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|------|
| GACGCGGTGA | TCGTGGTCTT | TGACGCCAAG | GCCCCCTCCT | TCCGCCACGA | GGCCTACGGG | 240 |
| GGGTACAAGG | CGGGCCGGGC | CCCCACGCCG | GAGGACTTTC | CCCGGCAACT | CGCCCTCATC | 300 |
| AAGGAGCTGG | TGGACCTCCT | GGGGCTGGCG | CGCCTCGAGG | TCCCGGGCTA | CGAGGCGGAC | 360 |
| GACGTCTTGG | CCAGCCTGGC | CAAGAAGGCG | GAAAAGGAGG | GCTACGAGGT | CCGCATCCTC | 420 |
| ACCGCCGACA | AAGACCTTTA | CCAGCTCCTT | TCCGACCGCA | TCCACGTCCT | CCACCCCGAG | 480 |
| GGGTACCTCA | TCACCCCGGC | CTGGCTTTGG | GAAAAGTACG | GCCTGAGGCC | CGACCAGTGG | 540 |
| GCCGACTACC | GGGCCCTGAC | CGGGGACGAG | TCCGACAACC | TTCCCGGGGT | CAAGGGCATC | 600 |
| GGGGAGAAGA | CGGCGAGGAA | GCTTCTGGAG | GAGTGGGGGA | GCCTGGAAGC | CCTCCTCAAG | 660 |
| AACCTGGACC | GGCTGAAGCC | CGCCATCCGG | GAGAAGATCC | TGGCCACAT | GGACGATCTG | 720 |
| AAGCTCTCCT | GGGACCTGGC | CAAGGTGCGC | ACCGACCTGC | CCCTGGAGGT | GGACTTCGCC | 780 |
| AAAAGGCGGG | AGCCCGACCG | GGAGAGGCTT | AGGGCCTTTC | TGGAGAGGCT | TGAGTTTGGC | 840 |
| AGCCTCCTCC | ACGAGTTCGG | CCTTCTGGAA | AGCCCCAAGG | CCCTGGAGGA | GGCCCCCTGG | 900 |
| CCCCCGCCGG | AAGGGGCCTT | CGTGGGCTTT | GTGCTTTCCC | GCAAGGAGCC | CATGTGGGCC | 960 |
| GATCTTCTGG | CCCTGGCCGC | CGCCAGGGGG | GGCCGGGTCC | ACCGGGCCCC | CGAGCCTTAT | 1020 |
| AAAGCCCTCA | GGGACCTGAA | GGAGGCGCGG | GGGCTTCTCG | CCAAAGACCT | GAGCGTTCTG | 1080 |
| GCCCTGAGGG | AAGGCCTTGG | CCTCCCGCCC | GGCGACGACC | CCATGCTCCT | CGCCTACCTC | 1140 |
| CTGGACCCTT | CCAACACCAC | CCCCGAGGGG | GTGGCCCGGC | GCTACGGCGG | GGAGTGGACG | 1200 |
| GAGGAGGCGG | GGGAGCGGGC | CGCCCTTTCC | GAGAGGCTCT | TCGCCAACCT | GTGGGGGAGG | 1260 |
| CTTGAGGGGG | AGGAGAGGCT | CCTTTGGCTT | TACCGGGAGG | TGGAGAGGCC | CCTTTCCGCT | 1320 |
| GTCCTGGCCC | ACATGGAGGC | CACGGGGGTG | CGCCTGGACG | TGGCCTATCT | CAGGGCCTTG | 1380 |
| TCCCTGGAGG | TGGCCGGGGA | GATCGCCCGC | CTCGAGGCCG | AGGTCTTCCG | CCTGGCCGGC | 1440 |
| CACCCCTTCA | ACCTCAACTC | CCGGGACCAG | CTGGAAAGGG | TCCTCTTTGA | CGAGCTAGGG | 1500 |
| CTTCCCGCCA | TCGGCAAGAC | GGAGAAGACC | GGCAAGCGCT | CCACCAGCGC | CGCCGTCCTG | 1560 |
| GAGGCCCTCC | GCGAGGCCCA | CCCCATCGTG | GAGAAGATCC | TGCAGTACCG | GGAGCTCACC | 1620 |
| AAGCTGAAGA | GCACCTACAT | TGACCCCTTG | CCGGACCTCA | TCCACCCAG | GACGGGCCGC | 1680 |
| CTCCACACCC | GCTTCAACCA | GACGGCCACG | GCCACGGGCA | GGCTAAGTAG | CTCCGATCCC | 1740 |
| AACCTCCAGA | ACATCCCCGT | CCGCACCCCG | CTTGGGCAGA | GGATCCGCCG | GGCCTTCATC | 1800 |
| GCCGAGGAGG | GGTGGCTATT | GGTGGCCCTG | GA CTATAGCC | AGATAGAGCT | CAGGGTGCTG | 1860 |
| GCCCACCTCT | CCGGCGACGA | GAACCTGATC | CGGGTCTTCC | AGGAGGGGCG | GGACATCCAC | 1920 |
| ACGGAGACCG | CCAGCTGGAT | GTTCGGCGTC | CCCCGGGAGG | CCGTGGACCC | CCTGATGCGC | 1980 |
| CGGGCGGCCA | AGACCATCAA | CTTCGGGGTC | CTCTACGGCA | TGTCGGCCCA | CCGCCTCTCC | 2040 |

CAGGAGCTAG CTAGCCATCC CTTACGAGGA GGCCAGGCC TTCATTGA

2088

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGAATTCGG GGATGCTGCC CCTCTTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC 60
CACCACCTGG CCTACGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAG CCGGGGGGAG 120
CCGGTGCAGG CGGTCTACGG CTTGCGCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG 180
GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG 240
GGGTACAAGG CGGGCCGGGC CCCACGCCG GAGGACTTTC CCCGGCAACT CGCCCTCATC 300
AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCGGGCTA CGAGGCGGAC 360
GACGTCCTGG CCAGCCTGGC CAAGAAGGCG GAAAAGGAGG GCTACGAGGT CCGCATCCTC 420
ACCGCCGACA AAGACCTTTA CCAGCTTCTT TCCGACCGCA TCCACGTCCT CCACCCCGAG 480
GGGTACCTCA TCACCCCGGC CTGGCTTTGG GAAAAGTACG GCCTGAGGCC CGACCAGTGG 540
GCCGACTACC GGGCCCTGAC CGGGGACGAG TCCGACAACC TTCCCGGGGT CAAGGGCATC 600
GGGGAGAAGA CGGCGAGGAA GCTTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG 660
AACCTGGACC GGCTGAAGCC CGCCATCCGG GAGAAGATCC TGGCCACAT GGACGATCTG 720
AAGCTCTCCT GGGACCTGGC CAAGGTGCGC ACCGACCTGC CCCTGGAGGT GGACTTCGCC 780
AAAAGGCGGG AGCCCGACCG GGAGAGGCTT AGGGCCTTTC TGGAGAGGCT TGAGTTTGGC 840
AGCCTCCTCC ACGAGTTCGG CCTTCTGGAA AGCCCCAAGT CATGGAGGGG GTGTATCCCC 900
TGGCCGTGCC CTTGGAGGTG GAGGTGGGGA TAGGGGAGGA CTGGCTCTCC GCCAAGGAGT 960
GA 962

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGGAATTCG GGGATGCTGC CCCTCTTTGA GCCCAAGGGC CGGGTCCTCC TGGTGGACGG 60

| | |
|--|------|
| CCACCACCTG GCCTACCGCA CCTTCCACGC CCTGAAGGGC CTCACCACCA GCCGGGGGGA | 120 |
| GCCGGTGCAG GCGGTCTACG GCTTCGCCAA GAGCCTCCTC AAGGCCCTCA AGGAGGACGG | 180 |
| GGACGCGGTG ATCGTGGTCT TTGACGCCAA GGCCCCCTCC TTCCGCCACG AGGCCTACGG | 240 |
| GGGGTACAAG GCGGGCCGGG CCCCCACGCC GGAGGACTTT CCCC GGCAAC TCGCCCTCAT | 300 |
| CAAGGAGCTG GTGGACCTCC TGGGGCTGGC GCGCCTCGAG GTCCCGGGCT ACGAGGCGGA | 360 |
| CGACGTCCTG GCCAGCCTGG CCAAGAAGGC GGAAAAGGAG GGCTACGAGG TCCGCATCCT | 420 |
| CACCGCCGAC AAAGACCTTT ACCAGCTCCT TTCCGACCGC ATCCACGTCC TCCACCCCGA | 480 |
| GGGGTACCTC ATCACCCCGG CCTGGCTTTG GGAAAAGTAC GGCCTGAGGC CCGACCAGTG | 540 |
| GGCCGACTAC CGGGCCCTGA CCGGGGACGA GTCCGACAAC CTTCCCGGGG TCAAGGGCAT | 600 |
| CGGGGAGAAG ACGGCGAGGA AGCTTCTGGA GGAGTGGGGG AGCCTGGAAG CCCTCCTCAA | 660 |
| GAACCTGGAC CGGCTGAAGC CCGCCATCCG GGAGAAGATC CTGGCCCACA TGGACGATCT | 720 |
| GAAGCTCTCC TGGGACCTGG CCAAGGTGCG CACCGACCTG CCCCTGGAGG TGGACTTCGC | 780 |
| CAAAAGGCGG GAGCCCGACC GGGAGAGGCT TAGGGCCTTT CTGGAGAGGC TTGAGTTTGG | 840 |
| CAGCCTCCTC CACGAGTTCG GCCTTCTGGA AAGCCCCAAG ATCCGCCGGG CCTTCATCGC | 900 |
| CGAGGAGGGG TGGCTATTGG TGGCCCTGGA CTATAGCCAG ATAGAGCTCA GGGTGCTGGC | 960 |
| CCACCTCTCC GGCACGAGA ACCTGATCCG GGTCTTCCAG GAGGGGCGGG ACATCCACAC | 1020 |
| GGAGACCGCC AGCTGGATGT TCGGCGTCCC CCGGGAGGCC GTGGACCCCC TGATGCGCCG | 1080 |
| GGCGGCCAAG ACCATCAACT TCGGGGTCTT CTACGGCATG TCGGCCACC GCCTCTCCCA | 1140 |
| GGAGCTAGCC ATCCCTTACG AGGAGGCCCA GGCCTTCATT GAGCGCTACT TTCAGAGCTT | 1200 |
| CCCCAAGGTG CGGGCCTGGA TTGAGAAGAC CCTGGAGGAG GGCAGGAGGC GGGGGTACGT | 1260 |
| GGAGACCCTC TTCGGCCGCC GCCGCTACGT GCCAGACCTA GAGGCCCGGG TGAAGAGCGT | 1320 |
| GCGGGAGGCG GCCGAGCGCA TGGCCTTCAA CATGCCCGTC CGGGGCACCG CCGCCGACCT | 1380 |
| CATGAAGCTG GCTATGGTGA AGCTCTTCCC CAGGCTGGAG GAAATGGGGG CCAGGATGCT | 1440 |
| CCTTCAGGTC CACGACGAGC TGGTCTCGA GGCCCCAAAA GAGAGGGCGG AGGCCGTGGC | 1500 |
| CCGGCTGGCC AAGGAGGTCA TGGAGGGGGT GTATCCCCTG GCCGTGCCCC TGGAGGTGGA | 1560 |
| GGTGGGGATA GGGGAGGACT GGCTCTCCGC CAAGGAGTGA | 1600 |

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CACGAATTCG GGGATGCTGC CCCTCTTTGA GCCCAA

36

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTGAGATCTA TCACTCCTTG GCGGAGAGCC AGTC

34

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TAATACGACT CACTATAGGG AGACCGGAAT TCGAGCTCGC CCGGGCGAGC TCGAATTCCG

60

TGTATTCTAT AGTGTACCT AAATCGAATT C

91

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TAATACGACT CACTATAGGG

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCGATT TAGGTGACAC TATAGAA

27

090419-082801 EST-1650

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTAATCATGG TCATAGCTGG TAGCTTGCTA C

31

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGATCCTCTA GAGTCGACCT GCAGGCATGC CTACCTTGGT AG

42

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGATCCTCTA GAGTCGACCT GCAGGCATGC

30

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGAATTTCGG GGATGCTGCC CCTCTTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC 60

CACCACCTGG CCTACCGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAG CCGGGGGGAG 120

CCGGTGCAGG CGGTCTACGG CTTGCCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG 180

GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG 240

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| GGGTACAAGG | CGGGCCGGGC | CCCCACGCCG | GAGGACTTTC | CCCGGCAACT | CGCCCTCATC | 300 |
| AAGGAGCTGG | TGGACCTCCT | GGGGCTGGCG | CGCCTCGAGG | TCCCGGGCTA | CGAGGCGGAC | 360 |
| GACGTCTTGG | CCAGCTTGGC | CAAGAAGGCG | GAAAAGGAGG | GCTACGAGGT | CCGCATCCTC | 420 |
| ACCGCCGACA | AAGACCTTTA | CCAGCTCCTT | TCCGACCGCA | TCCACGTCTT | CCACCCCGAG | 480 |
| GGGTACCTCA | TCACCCCGGC | CTGGCTTTGG | GAAAAGTACG | GCCTGAGGCC | CGACCAGTGG | 540 |
| GCCGACTACC | GGGCCCTGAC | CGGGGACGAG | TCCGACAACC | TTCCCGGGGT | CAAGGGCATC | 600 |
| GGGGAGAAGA | CGGCGAGGAA | GCTTCTGGAG | GAGTGGGGGA | GCCTGGAAGC | CCTCCTCAAG | 660 |
| AACCTGGACC | GGCTGAAGCC | CGCCATCCGG | GAGAAGATCC | TGGCCCACAT | GGACGATCTG | 720 |
| AAGCTCTCCT | GGGACCTGGC | CAAGGTGCGC | ACCGACCTGC | CCCTGGAGGT | GGACTTCGCC | 780 |
| AAAAGGCGGG | AGCCCGACCG | GGAGAGGCTT | AGGGCCTTTC | TGGAGAGGCT | TGAGTTTGGC | 840 |
| AGCCTCCTCC | ACGAGTTCGG | CCTTCTGGAA | AGCCCCAAGG | CCCTGGAGGA | GGCCCCCTGG | 900 |
| CCCCCGCCGG | AAGGGGCTTT | CGTGGGCTTT | GTGCTTTCCC | GCAAGGAGCC | CATGTGGGCC | 960 |
| GATCTTCTGG | CCCTGGCCGC | CGCCAGGGGG | GGCCGGGTCC | ACCGGGCCCC | CGAGCCTTAT | 1020 |
| AAAGCCCTCA | GGGACCTGAA | GGAGGCGCGG | GGGCTTCTCG | CCAAAGACCT | GAGCGTTCTG | 1080 |
| GCCCTGAGGG | AAGGCCTTGG | CCTCCCGCCC | GGCGACGACC | CCATGCTCCT | CGCCTACCTC | 1140 |
| CTGGACCCTT | CCAACACCAC | CCCCGAGGGG | GTGGCCCGGC | GCTACGGCGG | GGAGTGGACG | 1200 |
| GAGGAGGCGG | GGGAGCGGGC | CGCCCTTTCC | GAGAGGCTCT | TCGCCAACCT | GTGGGGGAGG | 1260 |
| CTTGAGGGGG | AGGAGAGGCT | CCTTTGGCTT | TACCGGGAGG | TGGAGAGGCC | CCTTTCCGCT | 1320 |
| GTCCTGGCCC | ACATGGAGGC | CACGGGGGTG | CGCCTGGACG | TGGCCTATCT | CAGGGCCTTG | 1380 |
| TCCCTGGAGG | TGGCCGGGGA | GATCGCCCGC | CTCGAGGCCG | AGGTCTTCCG | CCTGGCCGGC | 1440 |
| CACCCCTTCA | ACCTCAACTC | CCGGGACCAG | CTGGAAAGGG | TCCTCTTTGA | CGAGCTAGGG | 1500 |
| CTTCCCGCCA | TCGGCAAGAC | GGAGAAGACC | GGCAAGCGCT | CCACCAGCGC | CGCCGTCTTG | 1560 |
| GAGGCCCTCC | GCGAGGCCCA | CCCCATCGTG | GAGAAGATCC | TGCAGTACCG | GGAGCTCACC | 1620 |
| AAGCTGAAGA | GCACCTACAT | TGACCCCTTG | CCGGACCTCA | TCCACCCAG | GACGGGCCGC | 1680 |
| CTCCACACCC | GCTTCAACCA | GACGGCCACG | GCCACGGGCA | GGCTAAGTAG | CTCCGATCCC | 1740 |
| AACCTCCAGA | ACATCCCCGT | CCGCACCCCG | CTTGGGCAGA | GGATCCGCCG | GGCCTTCATC | 1800 |
| GCCGAGGAGG | GGTGGCTATT | GGTGGCCCTG | GACTATAGCC | AGATAGAGCT | CAGGGTGCTG | 1860 |
| GCCCACCTCT | CCGGCGACGA | GAACCTGATC | CGGGTCTTCC | AGGAGGGGCG | GGACATCCAC | 1920 |
| ACGGAGACCG | CCAGCTGGAT | GTTCCGGCGT | CCCCGGGAGG | CCGTGGACCC | CCTGATGCGC | 1980 |
| CGGGCGGCCA | AGACCATCAA | CTTCGGGGTC | CTCTACGGCA | TGTCGGCCCA | CCGCCTCTCC | 2040 |
| CAGGAGCTAG | CCATCCCTTA | CGAGGAGGCC | CAGGCCTTCA | TTGAGCGCTA | CTTTCAGAGC | 2100 |

TTCCCCAAGG TGCGGGCCTG GATTGAGAAG ACCCTGGAGG AGGGCAGGAG GCGGGGGTAC 2160
GTGGAGACCC TCTTCGGCCG CCGCCGCTAC GTGCCAGACC TAGAGGCCCCG GGTGAAGAGC 2220
GTGCGGGAGG CGGCCGAGCG CATGGCCTTC AACATGCCCG TCCGGGGCAC CGCCGCCGAC 2280
CTCATGAAGC TGGCTATGGT GAAGCTCTTC CCCAGGCTGG AGGAAATGGG GGCCAGGATG 2340
CTCCTTCAGG TCCACGACGA GCTGGTCCTC GAGGCCCCAA AAGAGAGGGC GGAGGCCGTG 2400
GCCCCGGCTGG CCAAGGAGGT CATGGAGGGG GTGTATCCCC TGGCCGTGCC CCTGGAGGTG 2460
GAGGTGGGGA TAGGGGAGGA CTGGCTCTCC GCCAAGGAGT GA 2502

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATTTAGGTG AACTATAG 19

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CGGACGAACA AGCGAGACAG CGACACAGGT ACCACATGGT ACAAGAGGCA AGAGAGACGA 60

CACAGCAGAA AC 72

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTTTCTGCTG TGTCGTCTCT CTTGCCTCTT GTACCATGTG GTACCTGTGT CGCTGTCTCG 60

CTTGTTTCGTC 70

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GACGAACAAG CGAGACAGCG

20

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTTTCTGCTG TGTCGTCTCT CTTG

24

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCTCTTGCTAC CATGTGGTAC CTGTGTCGCT GTCTCGCTTG TTCGTC

46

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ACACAGGTAC CACATGGTAC AAGAGGCAAG AGAGACGACA CAGCAGAAAC

50

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Met | Thr | Gly | Gly | Gln | Gln | Met | Gly | Arg | Ile | Asn | Ser |
| 1 | | | | 5 | | | | | 10 | | | | | 15 |

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

| | |
|--|-----|
| ATGGCTAGCA TGACTGGTGG ACAGCAAATG GGTCGGATCA ATTCGGGGAT GCTGCCCCCTC | 60 |
| TTTGAGCCCA AGGGCCGGGT CCTCCTGGTG GACGGCCACC ACCTGGCCTA CCGCACCTTC | 120 |
| CACGCCCTGA AGGGCCTCAC CACCAGCCGG GGGGAGCCGG TGCAGGCGGT CTACGGCTTC | 180 |
| GCCAAGAGCC TCCTCAAGGC CCTCAAGGAG GACGGGGACG CGGTGATCGT GGTCTTTGAC | 240 |
| GCCAAGGCCC CCTCCTTCCG CCACGAGGCC TACGGGGGGT ACAAGGCGGG CCGGGCCCCC | 300 |
| ACGCCGGAGG ACTTTCCCCG GCAACTCGCC CTCATCAAGG AGCTGGTGGA CCTCCTGGGG | 360 |
| CTGGCGCGCC TCGAGGTCCC GGGCTACGAG GCGGACGACG TCCTGGCCAG CCTGGCCAAG | 420 |
| AAGGCGGAAA AGGAGGGCTA CGAGGTCCGC ATCCTCACCG CCGACAAAGA CCTTTACCAG | 480 |
| CTTCTTTCCG ACCGCATCCA CGTCTCCAC CCCGAGGGGT ACCTCATCAC CCCGGCCTGG | 540 |
| CTTTGGGAAA AGTACGGCCT GAGGCCCGAC CAGTGGGCCG ACTACCGGGC CCTGACCGGG | 600 |
| GACGAGTCCG ACAACCTTCC CGGGGTCAAG GGCATCGGGG AGAAGACGGC GAGGAAGCTT | 660 |
| CTGGAGGAGT GGGGGAGCCT GGAAGCCCTC CTCAAGAACC TGGACCGGCT GAAGCCCCGCC | 720 |
| ATCCGGGAGA AGATCCTGGC CCACATGGAC GATCTGAAGC TCTCCTGGGA CCTGGCCAAG | 780 |
| GTGCGCACCG ACCTGCCCCT GGAGGTGGAC TTCGCCAAAA GGCGGGAGCC CGACCGGGAG | 840 |
| AGGCTTAGGG CCTTTCTGGA GAGGCTTGAG TTTGGCAGCC TCCTCCACGA GTTCGGCCTT | 900 |
| CTGGAAAGCC CCAAGTCATG GAGGGGGTGT ATCCCTGGC CGTGCCCTG GAGGTGGAGG | 960 |
| TGGGGATAG | 969 |

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 948 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

| | |
|--|-----|
| ATGGCTAGCA TGACTGGTGG ACAGCAAATG GGTCGGATCA ATTCGGGGAT GCTGCCCCCTC | 60 |
| TTTGAGCCCA AGGGCCGGGT CCTCCTGGTG GACGGCCACC ACCTGGCCTA CCGCACCTTC | 120 |
| CACGCCCTGA AGGGCCTCAC CACCAGCCGG GGGGAGCCGG TGCAGGCGGT CTACGGCTTC | 180 |
| GCCAAGAGCC TCCTCAAGGC CCTCAAGGAG GACGGGGACG CGGTGATCGT GGTCTTTGAC | 240 |
| GCCAAGGCCC CCTCCTTCCG CCACGAGGCC TACGGGGGGT ACAAGGCGGG CCGGGCCCCC | 300 |
| ACGCCGGAGG ACTTTCCCCG GCAACTCGCC CTCATCAAGG AGCTGGTGGA CCTCCTGGGG | 360 |
| CTGGCGCGCC TCGAGGTCCC GGGCTACGAG GCGGACGACG TCCTGGCCAG CCTGGCCAAG | 420 |
| AAGGCGGAAA AGGAGGGCTA CGAGGTCCGC ATCCTCACCG CCGACAAAGA CCTTTACCAG | 480 |
| CTTCTTTCCG ACCGCATCCA CGTCCTCCAC CCCGAGGGGT ACCTCATCAC CCCGGCCTGG | 540 |
| CTTTGGGAAA AGTACGGCCT GAGGCCCCGAC CAGTGGGCCG ACTACCGGGC CCTGACCGGG | 600 |
| GACGAGTCCG ACAACCTTCC CGGGGTCAAG GGCATCGGGG AGAAGACGGC GAGGAAGCTT | 660 |
| CTGGAGGAGT GGGGGAGCCT GGAAGCCCTC CTCAAGAACC TGGACCGGCT GAAGCCCGCC | 720 |
| ATCCGGGAGA AGATCCTGGC CCACATGGAC GATCTGAAGC TCTCCTGGGA CCTGGCCAAG | 780 |
| GTGCGCACC GACCTGCCCCCT GGAGGTGGAC TTCGCCAAAA GGCGGGAGCC CGACCGGGAG | 840 |
| AGGCTTAGGG CCTTTCTGGA GAGGCTTGAG TTTGGCAGCC TCCTCCACGA GTTCGGCCTT | 900 |
| CTGGAAAGCC CCAAGGCCGC ACTCGAGCAC CACCACCACC ACCACTGA | 948 |

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 206 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

| | |
|--|-----|
| CGCCAGGGTT TTCCCAGTCA CGACGTTGTA AAACGACGGC CAGTGAATTG TAATACGACT | 60 |
| CACTATAGGG CGAATTTCGAG CTCGGTACCC GGGGATCCTC TAGAGTCGAC CTGCAGGCAT | 120 |
| GCAAGCTTGA GTATTCTATA GTGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG | 180 |
| TTTCCTGTGT GAAATTGTGA TCCGCT | 206 |

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTCTGGGTTTCTCTGCTCTCTGGTCGCTGTC TCGCTTGTTTCTCTGTC

43

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCTGTCTCGCTTGTTCGTC

19

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GACGAACAAGCGAGACAGCG

20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTCTGGGTTTCTCTGCTCTCTGGTC

24

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GACGAACAAGCGAGACAGCGACAGAGAGCAGAGAACCCAGAA

43

03230"EST750

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ACCAGAGAGC AGAGAACCCA GAA

23

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AACAGCTATG ACCATGATTA C

21

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA

60

TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA

120

GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG

157

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTAGACA TAACCGGGAA

60

TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA

120

0943 0930

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

19

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TAGTGTTACC AATTTATTTT GAGATAACAC AAAACTTTA 339

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCCTTATTTT ACTTTAAAAA T

21

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TAAAGTTTTG TGTTATCTCA

20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA

60

TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA

120

GATCTGGGCT ATGACTATAG CTATCTACAA GATTGAC

157

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTTT GGATGAAATA AAGAAATCAC

60

CATTTCTGTA CAGTGGTATA AAAGGAACCA TGTAGGATTC CCGGTTATGT CCAATGGGTG

120

CATTGGCTTC TGGATAAACT TCTGAAGAG GACGGTG

157

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AGCGGATAAC AATTTACACAGGAAACAGC TATGACCATG ATTACGCCAA GCTATTTAGG 60
TGACACTATA GAATACTCAA GCTTGCATGC CTGCAGGTCG ACTCTAGAGG ATCCCCGGGT 120
ACCGAGCTCG AATTCGCCCT ATAGTGAGTC GTATTAGGAT CCGTG 165

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CGCCAGGGTT TTCCAGTCA CGACGTTGTA AAACGACGGC CAGTGAATTG TAATACGACT 60
CACTATAGGG CGAATTCGAG CTCGGTACCC GGGGATCCTC TAGAGTCGAC CTGCAGGCAT 120
GCAAGCTTGA GTATTCTATA GTGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG 180
TTTCCTGTGT GAAATTGTGA TCCGCT 206

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AGCGGATAAC AATTTACACAGGA 24

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CACGGATCCT AATACGACTC ACTATAGGG 29

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CGCCAGGGTT TTCCAGTCA CGAC

24

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

| | |
|---|-----|
| CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTAGACA TAACCGGGAA | 60 |
| TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA | 120 |
| GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG | 157 |

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

| | |
|---|-----|
| CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCAGGAA | 60 |
| TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA | 120 |
| GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG | 157 |

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

| | |
|---|----|
| CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA | 60 |
|---|----|

| | |
|---|-----|
| TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA | 120 |
| GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAGACC CAGACTCTTT TCAAGACTAC | 180 |
| ATTAAGTCCT ATTTGGAACA AGCGAGTCGG ATCTGGTCAT GGCTCCTTGG GCGGGCGATG | 240 |
| GTAGGGGCCG TCCTCACTGC CCTGCTGGCA GGGCTTGTGA GCTTGCTGTG TCGTCACAAG | 300 |
| AGAAAGCAGC TTCCTGAAGA AAAGCAGCCA CTCCTCATGG AGAAAGAGGA TTACCACAGC | 360 |
| TTGTATCAGA GCCATTTA | 378 |

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

| | |
|---|-----|
| CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCAGGAA | 60 |
| TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA | 120 |
| GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAGACC CAGACTCTTT TCAAGACTAC | 180 |
| ATTAAGTCCT ATTTGGAACA AGCGAGTCGG ATCTGGTCAT GGCTCCTTGG GCGGGCGATG | 240 |
| GTAGGGGCCG TCCTCACTGC CCTGCTGGCA GGGCTTGTGA GCTTGCTGTG TCGTCACAAG | 300 |
| AGAAAGCAGC TTCCTGAAGA AAAGCAGCCA CTCCTCATGG AGAAAGAGGA TTACCACAGC | 360 |
| TTGTATCAGA GCCATTTA | 378 |

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1059 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

| | |
|---|-----|
| GCAAGTTTGG CTTTTGGGGA CCAAACTGCA CAGAGAGACG ACTCTTGGTG AGAAGAAACA | 60 |
| TCTTCGATTT GAGTGCCCCA GAGAAGGACA AATTTTTTGC CTACCTCACT TTAGCAAAGC | 120 |
| ATACCATCAG CTCAGACTAT GTCATCCCCA TAGGGACCTA TGGCCAAATG AAAAATGGAT | 180 |
| CAACACCCAT GTTTAACGAC ATCAATATTT ATGACCTCTT TGTCTGGATG CATTATTATG | 240 |
| TGTCAATGGA TGCCTGCTT GGGGGATATG AAATCTGGAG AGACATTGAT TTTGCCCATG | 300 |
| AAGCACCAGC TTTTCTGCCT TGGCATAGAC TCTTCTTGTT GCGGTGGGAA CAAGAAATCC | 360 |

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AGAAGCTGAC AGGAGATGAA AACTTCACTA TTCCATATTG GGACTGGCGG GATGCAGAAA 420
 AGTGTGACAT TTGCACAGAT GAGTACATGG GAGGTCAGCA CCCCACAAAT CCTAACTTAC 480
 TCAGCCCAGC ATCATTCTTC TCCTCTTGGC AGATTGTCTG TAGCCGATTG GAGGAGTACA 540
 ACAGCCATCA GTCTTTATGC AATGGAACGC CCGAGGGACC TTTACGGCGT AATCCTGGAA 600
 ACCATGACAA ATCCAGAACC CCAAGGCTCC CCTCTTCAGC TGATGTAGAA TTTTGCCTGA 660
 GTTTGACCCA ATATGAATCT GGTTCATGG ATAAAGCTGC CAATTTTCAGC TTTAGAAATA 720
 CACTGGAAGG ATTTGCTAGT CCACTTACTG GGATAGCGGA TGCCTCTCAA AGCAGCATGC 780
 ACAATGCCTT GCACATCTAT ATGAATGGAA CAATGTCCCA GGTACAGGGA TCTGCCAACG 840
 ATCCTATCTT CCTTCTTCAC CATGCATTTG TTGACAGTAT TTTTGAGCAG TGGCTCCGAA 900
 GGCACCGTCC TCTTCAAGAA GTTTATCCAG AAGCCAATGC ACCCATTGGA CATAACCGGG 960
 AATCCTACAT GGTTCCTTTT ATACCACTGT ACAGAAATGG TGATTTCTTT ATTTTCATCCA 1020
 AAGATCTGGG CTATGACTAT AGCTATCTAC AAGATTCAG 1059

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1059 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCAAGTTTGG CTTTTGGGGA CCAAACCTGCA CAGAGAGACG ACTCTTGGTG AGAAGAAACA 60
 TCTTCGATTT GAGTGCCCCA GAGAAGGACA AATTTTTTGC CTACCTCACT TTAGCAAAGC 120
 ATACCATCAG CTCAGACTAT GTCATCCCCA TAGGGACCTA TGGCCAAATG AAAAATGGAT 180
 CAACACCCAT GTTTAACGAC ATCAATATTT ATGACCTCTT TGTCTGGATG CATTATTATG 240
 TGTCAATGGA TGCACCTGCTT GGGGGATATG AAATCTGGAG AGACATTGAT TTTGCCCATG 300
 AAGCACCAGC TTTTCTGCCT TGGCATAGAC TCTTCTTGTT GCGGTGGGAA CAAGAAATCC 360
 AGAAGCTGAC AGGAGATGAA AACTTCACTA TTCCATATTG GGACTGGCGG GATGCAGAAA 420
 AGTGTGACAT TTGCACAGAT GAGTACATGG GAGGTCAGCA CCCCACAAAT CCTAACTTAC 480
 TCAGCCCAGC ATCATTCTTC TCCTCTTGGC AGATTGTCTG TAGCCGATTG GAGGAGTACA 540
 ACAGCCATCA GTCTTTATGC AATGGAACGC CCGAGGGACC TTTACGGCGT AATCCTGGAA 600
 ACCATGACAA ATCCAGAACC CCAAGGCTCC CCTCTTCAGC TGATGTAGAA TTTTGCCTGA 660
 GTTTGACCCA ATATGAATCT GGTTCATGG ATAAAGCTGC CAATTTTCAGC TTTAGAAATA 720
 CACTGGAAGG ATTTGCTAGT CCACTTACTG GGATAGCGGA TGCCTCTCAA AGCAGCATGC 780

| | |
|--|------|
| ACAATGCCTT GCACATCTAT ATGAATGGAA CAATGTCCCA GGTACAGGGA TCTGCCAACG | 840 |
| ATCCTATCTT CTTCTTCAC CATGCATTTG TTGACAGTAT TTTTGAGCAG TGGCTCCGAA | 900 |
| GGCACCGTCC TCTTCAAGAA GTTTATCCAG AAGCCAATGC ACCCATGGA CATAACCAGG | 960 |
| AATCCTACAT GGTTCCTTTT ATACCACTGT ACAGAAATGG TGATTTCTTT ATTTTCATCCA | 1020 |
| AAGATCTGGG CTATGACTAT AGCTATCTAC AAGATTCAG | 1059 |

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1587 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

| | |
|--|------|
| ATGCTCCTGG CTGTTTGTGTA CTGCCTGCTG TGGAGTTTCC AGACCTCCGC TGGCCATTTT | 60 |
| CCTAGAGCCT GTGTCTCCTC TAAGAACCTG ATGGAGAAGG AATGCTGTCC ACCGTGGAGC | 120 |
| GGGGACAGGA GTCCCTGTGG CCAGCTTTCA GGCAGAGGTT CCTGTCAGAA TATCCTTCTG | 180 |
| TCCAATGCAC CACTTGGGCC TCAATTCCC TTCACAGGGG TGGATGACCG GGAGTCGTGG | 240 |
| CCTTCCGTCT TTTATAATAG GACCTGCCAG TGCTCTGGCA ACTTCATGGG ATTCAACTGT | 300 |
| GGAAACTGCA AGTTTGGCTT TTGGGGACCA AACTGCACAG AGAGACGACT CTTGGTGAGA | 360 |
| AGAAACATCT TCGATTTGAG TGCCCCAGAG AAGGACAAAT TTTTGCCTA CCTCACTTTA | 420 |
| GCAAAGCATA CCATCAGCTC AGACTATGTC ATCCCCATAG GGACCTATGG CCAAATGAAA | 480 |
| AATGGATCAA CACCCATGTT TAACGACATC AATATTTATG ACCTCTTTGT CTGGATGCAT | 540 |
| TATTATGTGT CAATGGATGC ACTGCTTGGG GGATATGAAA TCTGGAGAGA CATTGATTTT | 600 |
| GCCCATGAAG CACCAGCTTT TCTGCCTTGG CATAGACTCT TCTTGTGCG GTGGGAACAA | 660 |
| GAAATCCAGA AGCTGACAGG AGATGAAAAC TTCACTATTC CATATTGGGA CTGGCGGGAT | 720 |
| GCAGAAAAGT GTGACATTTG CACAGATGAG TACATGGGAG GTCAGCACCC CACAAATCCT | 780 |
| AACTTACTCA GCCCAGCATC ATTCTTCTCC TCTTGGCAGA TTGTCTGTAG CCGATTGGAG | 840 |
| GAGTACAACA GCCATCAGTC TTTATGCAAT GGAACGCCCG AGGGACCTTT ACGGCGTAAT | 900 |
| CCTGGAAACC ATGACAAATC CAGAACCCCA AGGCTCCCCT CTTCAGCTGA TGTAGAATTT | 960 |
| TGCCCTGAGTT TGACCCAATA TGAATCTGGT TCCATGGATA AAGCTGCCAA TTTCAGCTTT | 1020 |
| AGAAATACAC TGGAAGGATT TGCTAGTCCA CTTACTGGGA TAGCGGATGC CTCTCAAAGC | 1080 |
| AGCATGCACA ATGCCTTGCA CATCTATATG AATGGAACAA TGTCCCAGGT ACAGGGATCT | 1140 |
| GCCAACGATC CTATCTTCCT TCTTCACCAT GCATTTGTTG ACAGTATTTT TGAGCAGTGG | 1200 |

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| | |
|---|------|
| CTCCGAAGGC ACCGTCCTCT TCAAGAAGTT TATCCAGAAG CCAATGCACC CATTGGACAT | 1260 |
| AACCGGGAAT CCTACATGGT TCCTTTTATA CCACTGTACA GAAATGGTGA TTTCTTTATT | 1320 |
| TCATCCAAAG ATCTGGGCTA TGACTATAGC TATCTACAAG ATTCAGACCC AGACTCTTTT | 1380 |
| CAAGACTACA TTAAGTCCTA TTTGGAACAA GCGAGTCGGA TCTGGTCATG GCTCCTTGGG | 1440 |
| GCGGCGATGG TAGGGGCCGT CCTCACTGCC CTGCTGGCAG GGCTTGTGAG CTTGCTGTGT | 1500 |
| CGTCACAAGA GAAAGCAGCT TCCTGAAGAA AAGCAGCCAC TCCTCATGGA GAAAGAGGAT | 1560 |
| TACCACAGCT TGTATCAGAG CCATTTA | 1587 |

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

| | |
|---|------|
| ATGCTCCTGG CTGTTTTGTA CTGCCTGCTG TGGAGTTTCC AGACCTCCGC TGGCCATTTC | 60 |
| CCTAGAGCCT GTGTCTCCTC TAAGAACCTG ATGGAGAAGG AATGCTGTCC ACCGTGGAGC | 120 |
| GGGGACAGGA GTCCCTGTGG CCAGCTTTCA GGCAGAGGTT CCTGTCAGAA TATCCTTCTG | 180 |
| TCCAATGCAC CACTTGGGCC TCAATTTCCC TTCACAGGGG TGGATGACCG GGAGTCGTGG | 240 |
| CCTTCCGTCT TTTATAATAG GACCTGCCAG TGCTCTGGCA ACTTCATGGG ATTCAACTGT | 300 |
| GGAAACTGCA AGTTTGGCTT TTGGGGACCA AACTGCACAG AGAGACGACT CTTGGTGAGA | 360 |
| AGAAACATCT TCGATTGAG TGCCCCAGAG AAGGACAAAT TTTTGCCTA CCTCACTTTA | 420 |
| GCAAAGCATA CCATCAGCTC AGACTATGTC ATCCCCATAG GGACCTATGG CCAAATGAAA | 480 |
| AATGGATCAA CACCCATGTT TAACGACATC AATATTTATG ACCTCTTGT CTGGATGCAT | 540 |
| TATTATGTGT CAATGGATGC ACTGCTTGGG GGATATGAAA TCTGGAGAGA CATTGATTTT | 600 |
| GCCCATGAAG CACCAGCTTT TCTGCCTTGG CATAGACTCT TCTTGTGCG GTGGGAACAA | 660 |
| GAAATCCAGA AGCTGACAGG AGATGAAAAC TTCACTATTC CATATTGGGA CTGGCGGGAT | 720 |
| GCAGAAAAGT GTGACATTTG CACAGATGAG TACATGGGAG GTCAGCACCC CACAAATCCT | 780 |
| AACTTACTCA GCCCAGCATC ATTCTTCTCC TCTTGGCAGA TTGTCTGTAG CCGATTGGAG | 840 |
| GAGTACAACA GCCATCAGTC TTTATGCAAT GGAACGCCCG AGGGACCTTT ACGGCGTAAT | 900 |
| CCTGGAAACC ATGACAAATC CAGAACCCCA AGGCTCCCCT CTTCAGCTGA TGTAGAATTT | 960 |
| TGCCTGAGTT TGACCCAATA TGAATCTGGT TCCATGGATA AAGCTGCCAA TTTCAGCTTT | 1020 |
| AGAAATACAC TGGAAGGATT TGCTAGTCCA CTTACTGGGA TAGCGGATGC CTCTCAAAGC | 1080 |

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AGCATGCACA ATGCCTTGCA CATCTATATG AATGGAACAA TGTCCCAGGT ACAGGGATCT 1140
 GCCAACGATC CTATCTTCCT TCTTCACCAT GCATTTGTTG ACAGTATTTT TGAGCAGTGG 1200
 CTCCGAAGGC ACCGTCCTCT TCAAGAAGTT TATCCAGAAG CCAATGCACC CATTGGACAT 1260
 AACCAGGAAT CCTACATGGT TCCTTTTATA CCACTGTACA GAAATGGTGA TTTCTTTATT 1320
 TCATCCAAAG ATCTGGGCTA TGACTATAGC TATCTACAAG ATTCAGACCC AGACTCTTTT 1380
 CAAGACTACA TTAAGTCCTA TTTGGAACAA GCGAGTCGGA TCTGGTCATG GCTCCTTGGG 1440
 GCGGCGATGG TAGGGGCCGT CCTCACTGCC CTGCTGGCAG GGCTTGTGAG CTTGCTGTGT 1500
 CGTCACAAGA GAAAGCAGCT TCCTGAAGAA AAGCAGCCAC TCCTCATGGA GAAAGAGGAT 1560
 TACCACAGCT TGTATCAGAG CCATTTA 1587

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TAAATGGCTC TGATACAAGC T 21

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCAAGTTTGG CTTTGGGGA 20

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ATGCTCCTGG CTGTTTGTGTA CTG 23

(2) INFORMATION FOR SEQ ID NO:65:

009419 082301
100230 051460

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTTT GGATGAAATA AAGAAATCAC 60
CATTTCTGTA CAGTGGTATA AAAGGAACCA TGTAGGATTC CCGGTTATGT CTAATGGGTG 120
CATTGGCTTC TGGATAAACT TCTTGAAGAG GACGGTG 157

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTTT GGATGAAATA AAGAAATCAC 60
CATTTCTGTA CAGTGGTATA AAAGGAACCA TGTAGGATTC CTGGTTATGT CCAATGGGTG 120
CATTGGCTTC TGGATAAACT TCTTGAAGAG GACGGTG 157

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GGTTGGCCAA TCTACTCCCA GG 22

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GCTCACTCAG TGTGGCAAAG 20

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 536 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

| | |
|---|-----|
| GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC | 60 |
| AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT | 120 |
| CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG | 180 |
| GGCAAGGTGA ACGTGGATGA AGTTGGTGGT GAGGCCCTGG GCAGGTTGGT ATCAAGGTTA | 240 |
| CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG | 300 |
| GTTTCTGATA GGCCTGACT CTCTCTGCCT ATTGGTCTAT TTTCCACCC TTAGGCTGCT | 360 |
| GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA | 420 |
| TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTTAG | 480 |
| TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC | 536 |

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 534 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

| | |
|---|-----|
| GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC | 60 |
| AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT | 120 |
| CAAACAGACA CCATGGTGCA TCTGACTCCT GAGGAGGTCT GCCGTTACTG CCCTGTGGGG | 180 |
| CAAGGTGAAC GTGGATGAAG TTGGTGGTGA GGCCCTGGGC AGGTTGGTAT CAAGGTTACA | 240 |
| AGACAGGTTT AAGGAGACCA ATAGAACTG GGCATGTGGA GACAGAGAAG ACTCTTGGGT | 300 |
| TTCTGATAGG CACTGACTCT CTCTGCCTAT TGGTCTATTT TCCCACCCTT AGGCTGCTGG | 360 |
| TGGTCTACCC TTGGACCCAG AGGTTCTTTG AGTCCTTTGG GGATCTGTCC ACTCCTGATG | 420 |
| CTGTTATGGG CAACCCTAAG GTGAAGGCTC ATGGCAAGAA AGTGCTCGGT GCCTTTAGTG | 480 |
| ATGGCCTGGC TCACCTGGAC AACCTCAAGG GCACCTTTGC CACACTGAGT GAGC | 534 |

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 536 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

| | |
|---|-----|
| GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC | 60 |
| AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT | 120 |
| CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG | 180 |
| GGCAAGGTGA ACGTGGATGA AGTTGGTGGT GAGGCCCTGG GCAGGTTGGT ATCAAGGTTA | 240 |
| CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG | 300 |
| GTTTCTGATA GGCCTGACT CTCTCTGCCT ATTGGTCTAT TTTCCCACCC TTAGGCTGCT | 360 |
| GGTGGTCTAC CCTTGGACCT AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA | 420 |
| TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTTAG | 480 |
| TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC | 536 |

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 536 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

| | |
|---|-----|
| GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC | 60 |
| AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT | 120 |
| CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG | 180 |
| GGCAAGGTGA ACGTGGATGA AGTTGGAGGT GAGGCCCTGG GCAGGTTGGT ATCAAGGTTA | 240 |
| CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG | 300 |
| GTTTCTGATA GGCCTGACT CTCTCTGCCT ATTGGTCTAT TTTCCCACCC TTAGGCTGCT | 360 |
| GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA | 420 |
| TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTTAG | 480 |
| TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC | 536 |

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs

ATTTTAGAAG TAGGCCAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G

351

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

| | |
|---|-----|
| GGCTGACAAG AAGGAACTC GCTGAGATAG CAGGGACTTT CCACAAGGGG ATGTTATGGG | 60 |
| GAGGAGCCCG TCGGGAACAC CCACTTTCTT GATGTATAAA TATCACTGCA TTTCGCTCTG | 120 |
| TATTCAGTCG CTCTGCGGAG AGGCTGGCAG ATTGAGCCCT GGGAGGTTCT CTCCAGCACT | 180 |
| AGCAGGTAGA GCCTGGGTGT TCCCTGCTAG ACTCTACCA GCACTTAGCC AGTGCTGGGC | 240 |
| AGAGTGGCTC CACGCTTGCT TGCTTAAAGA CCTCTTCAAT AAAGCTGCCA TTTTAGAAGT | 300 |
| AAGCCAGTGT GTGTTCCCAT CTCTCCTAGC CGCCGCCTGG | 340 |

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

| | |
|---|-----|
| GGCTGACAAG AAGGAACTC GCTGAGATAG CAGGGACTTT CCACAAGGGG ATGTTATGGG | 60 |
| GAGGAGCCCG TCGGGAACAC CCACTTTCTT GGTGTATAAA TATCACTGCA TTTCGCTCTG | 120 |
| TATTCAGTCG CTCTGCGGAG AGGCTGGCAG ATTGAGCCCT GGGAGGTTCT CTCCAGCACT | 180 |
| AGCAGGTAGA GCCTGGGTGT TCCCTGCTAG ACTCTACCA GCACTTGGCC AGTGCTGGGC | 240 |
| AGAGTGGCTC CACGCTTGCT TGCTTAAAGA CCTCTTCAAT AAAGCTGCCA TTTTAGAAGT | 300 |
| AAGCCAGTGT GTGTTCCCAT CTCTCCTAGC CGCCGCCTGG | 340 |

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

094193 082301
T02230 561160

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 536 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

| | |
|---|-----|
| GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC | 60 |
| AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT | 120 |
| CAAACAGACA CCATGGTGCA TCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG | 180 |
| GGCAAGGTGA ACGTGGATGA AGTTGGTGGT AAGGCCCTGG GCAGGTGGT ATCAAGGTTA | 240 |
| CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG | 300 |
| GTTTCTGATA GGCCTGACT CTCTCTGCCT ATTGGTCTAT TTTCCACCC TTAGGCTGCT | 360 |
| GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA | 420 |
| TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTTAG | 480 |
| TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC | 536 |

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 536 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

| | |
|---|-----|
| GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC | 60 |
| AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT | 120 |
| CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG | 180 |
| GGCAAGGTGA ACGTGGATGA AGTTGGTGGT GAGGCCCTGG GCAGGTGGT ATCAAGGTTA | 240 |
| CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG | 300 |
| GTTTCTGATA GGCCTGACT CTCTCTGCCT ATTAGTCTAT TTTCCACCC TTAGGCTGCT | 360 |
| GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA | 420 |
| TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTTAG | 480 |
| TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC | 536 |

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```
CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCAGGAA      60
TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA      120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG                                157
```

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 833 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1          5          10          15
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20          25          30
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35          40          45
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50          55          60
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65          70          75          80
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85          90          95
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
100         105         110
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115         120         125
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130         135         140
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145         150         155         160
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165         170         175
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180         185         190
```


| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| Asn | Leu | Pro | Gly | Val | Lys | Gly | Ile | Gly | Glu | Lys | Thr | Ala | Arg | Lys | Leu | | |
| | | 195 | | | | | | 200 | | | | | | 205 | | | |
| Leu | Glu | Glu | Trp | Gly | Ser | Leu | Glu | Ala | Leu | Leu | Lys | Asn | Leu | Asp | Arg | | |
| | 210 | | | | | 215 | | | | | 220 | | | | | | |
| Leu | Lys | Pro | Ala | Ile | Arg | Glu | Lys | Ile | Leu | Ala | His | Met | Asp | Asp | Leu | | |
| 225 | | | | | 230 | | | | | 235 | | | | | | | 240 |
| Lys | Leu | Ser | Trp | Asp | Leu | Ala | Lys | Val | Arg | Thr | Asp | Leu | Pro | Leu | Glu | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | |
| Val | Asp | Phe | Ala | Lys | Arg | Arg | Glu | Pro | Asp | Arg | Glu | Arg | Leu | Arg | Ala | | |
| | | | 260 | | | | | 265 | | | | | 270 | | | | |
| Phe | Leu | Glu | Arg | Leu | Glu | Phe | Gly | Ser | Leu | Leu | His | Glu | Phe | Gly | Leu | | |
| | 275 | | | | | | 280 | | | | | 285 | | | | | |
| Leu | Glu | Ser | Pro | Lys | Ala | Leu | Glu | Glu | Ala | Pro | Trp | Pro | Pro | Pro | Glu | | |
| 290 | | | | | | 295 | | | | | 300 | | | | | | |
| Gly | Ala | Phe | Val | Gly | Phe | Val | Leu | Ser | Arg | Lys | Glu | Pro | Met | Trp | Ala | | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | | |
| Asp | Leu | Leu | Ala | Leu | Ala | Ala | Ala | Arg | Gly | Gly | Arg | Val | His | Arg | Ala | | |
| | | | | 325 | | | | | 330 | | | | | 335 | | | |
| Pro | Glu | Pro | Tyr | Lys | Ala | Leu | Arg | Asp | Leu | Lys | Glu | Ala | Arg | Gly | Leu | | |
| | | | 340 | | | | | 345 | | | | | 350 | | | | |
| Leu | Ala | Lys | Asp | Leu | Ser | Val | Leu | Ala | Leu | Arg | Glu | Gly | Leu | Gly | Leu | | |
| | | 355 | | | | | 360 | | | | | 365 | | | | | |
| Pro | Pro | Gly | Asp | Asp | Pro | Met | Leu | Leu | Ala | Tyr | Leu | Leu | Asp | Pro | Ser | | |
| | 370 | | | | | 375 | | | | | 380 | | | | | | |
| Asn | Thr | Thr | Pro | Glu | Gly | Val | Ala | Arg | Arg | Tyr | Gly | Gly | Glu | Trp | Thr | | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | | |
| Glu | Glu | Ala | Gly | Glu | Arg | Ala | Ala | Leu | Ser | Glu | Arg | Leu | Phe | Ala | Asn | | |
| | | | | 405 | | | | | 410 | | | | | 415 | | | |
| Leu | Trp | Gly | Arg | Leu | Glu | Gly | Glu | Glu | Arg | Leu | Leu | Trp | Leu | Tyr | Arg | | |
| | | | 420 | | | | | 425 | | | | | 430 | | | | |
| Glu | Val | Glu | Arg | Pro | Leu | Ser | Ala | Val | Leu | Ala | His | Met | Glu | Ala | Thr | | |
| | | 435 | | | | | 440 | | | | | 445 | | | | | |
| Gly | Val | Arg | Leu | Asp | Val | Ala | Tyr | Leu | Arg | Ala | Leu | Ser | Leu | Glu | Val | | |
| | 450 | | | | | 455 | | | | | 460 | | | | | | |
| Ala | Gly | Glu | Ile | Ala | Arg | Leu | Glu | Ala | Glu | Val | Phe | Arg | Leu | Ala | Gly | | |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 | | |
| His | Pro | Phe | Asn | Leu | Asn | Ser | Arg | Asp | Gln | Leu | Glu | Arg | Val | Leu | Phe | | |
| | | | | 485 | | | | | 490 | | | | | 495 | | | |
| Asp | Glu | Leu | Gly | Leu | Pro | Ala | Ile | Gly | Lys | Thr | G | | | | | | |

0954193-082801

Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
580 585 590

Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
625 630 635 640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
675 680 685

Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
740 745 750

Pro Val Arg Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
770 775 780

His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 548 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Ser | Gly | Met | Leu | Pro | Leu | Phe | Glu | Pro | Lys | Gly | Arg | Val | Leu | 1 | 5 | 10 | 15 |
| Leu | Val | Asp | Gly | His | His | Leu | Ala | Tyr | Arg | Thr | Phe | His | Ala | Leu | Lys | 20 | 25 | 30 | |
| Gly | Leu | Thr | Thr | Ser | Arg | Gly | Glu | Pro | Val | Gln | Ala | Val | Tyr | Gly | Phe | 35 | 40 | 45 | |
| Ala | Lys | Ser | Leu | Leu | Lys | Ala | Leu | Lys | Glu | Asp | Gly | Asp | Ala | Val | Ile | 50 | 55 | 60 | |
| Val | Val | Phe | Asp | Ala | Lys | Ala | Pro | Ser | Phe | Arg | His | Glu | Ala | Tyr | Gly | 65 | 70 | 75 | 80 |
| Gly | Tyr | Lys | Ala | Gly | Arg | Ala | Pro | Thr | Pro | Glu | Asp | Phe | Pro | Arg | Gln | 85 | 90 | 95 | |
| Leu | Ala | Leu | Ile | Lys | Glu | Leu | Val | Asp | Leu | Leu | Gly | Leu | Ala | Arg | Leu | 100 | 105 | 110 | |
| Glu | Val | Pro | Gly | Tyr | Glu | Ala | Asp | Asp | Val | Leu | Ala | Ser | Leu | Ala | Lys | 115 | 120 | 125 | |
| Lys | Ala | Glu | Lys | Glu | Gly | Tyr | Glu | Val | Arg | Ile | Leu | Thr | Ala | Asp | Lys | 130 | 135 | 140 | |
| Asp | Leu | Tyr | Gln | Leu | Leu | Ser | Asp | Arg | Ile | His | Val | Leu | His | Pro | Glu | 145 | 150 | 155 | 160 |
| Gly | Tyr | Leu | Ile | Thr | Pro | Ala | Trp | Leu | Trp | Glu | Lys | Tyr | Gly | Leu | Arg | 165 | 170 | 175 | |
| Pro | Asp | Gln | Trp | Ala | Asp | Tyr | Arg | Ala | Leu | Thr | Gly | Asp | Glu | Ser | Asp | 180 | 185 | 190 | |
| Asn | Leu | Pro | Gly | Val | Lys | Gly | Ile | Gly | Glu | Lys | Thr | Ala | Arg | Lys | Leu | 195 | 200 | 205 | |
| Leu | Glu | Glu | Trp | Gly | Ser | Leu | Glu | Ala | Leu | Leu | Lys | Asn | Leu | Asp | Arg | 210 | 215 | 220 | |
| Leu | Lys | Pro | Ala | Ile | Arg | Glu | Lys | Ile | Leu | Ala | His | Met | Asp | Asp | Leu | 225 | 230 | 235 | 240 |
| Lys | Leu | Ser | Trp | Asp | Leu | Ala | Lys | Val | Arg | Thr | Asp | Leu | Pro | Leu | Glu | 245 | 250 | 255 | |
| Val | Asp | Phe | Ala | Lys | Arg | Arg | Glu | Pro | Asp | Arg | Glu | Arg | Leu | Arg | Ala | 260 | 265 | 270 | |
| Phe | Leu | Glu | Arg | Leu | Glu | Phe | Gly | Ser | Leu | Leu | His | Glu | Phe | Gly | Leu | 275 | 280 | 285 | |

0994193-082801

009419-032301

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
325 330 335

Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
340 345 350

Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
355 360 365

Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
385 390 395 400

Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
405 410 415

Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
420 425 430

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
435 440 445

Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
450 455 460

Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
515 520 525

Ile Val Glu Lys Ile Leu Gln Ala Cys Lys Leu Gly Thr Gly Arg Arg
530 535 540

Phe Thr Thr Ser
545

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

1002280" E6TF4650

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Ser | Gly | Met | Leu | Pro | Leu | Phe | Glu | Pro | Lys | Gly | Arg | Val | Leu | 1 | 5 | 10 | 15 |
| Leu | Val | Asp | Gly | His | His | Leu | Ala | Tyr | Arg | Thr | Phe | His | Ala | Leu | Lys | 20 | 25 | 30 | |
| Gly | Leu | Thr | Thr | Ser | Arg | Gly | Glu | Pro | Val | Gln | Ala | Val | Tyr | Gly | Phe | 35 | 40 | 45 | |
| Ala | Lys | Ser | Leu | Leu | Lys | Ala | Leu | Lys | Glu | Asp | Gly | Asp | Ala | Val | Ile | 50 | 55 | 60 | |
| Val | Val | Phe | Asp | Ala | Lys | Ala | Pro | Ser | Phe | Arg | His | Glu | Ala | Tyr | Gly | 65 | 70 | 75 | 80 |
| Gly | Tyr | Lys | Ala | Gly | Arg | Ala | Pro | Thr | Pro | Glu | Asp | Phe | Pro | Arg | Gln | 85 | 90 | 95 | |
| Leu | Ala | Leu | Ile | Lys | Glu | Leu | Val | Asp | Leu | Leu | Gly | Leu | Ala | Arg | Leu | 100 | 105 | 110 | |
| Glu | Val | Pro | Gly | Tyr | Glu | Ala | Asp | Asp | Val | Leu | Ala | Ser | Leu | Ala | Lys | 115 | 120 | 125 | |
| Lys | Ala | Glu | Lys | Glu | Gly | Tyr | Glu | Val | Arg | Ile | Leu | Thr | Ala | Asp | Lys | 130 | 135 | 140 | |
| Asp | Leu | Tyr | Gln | Leu | Leu | Ser | Asp | Arg | Ile | His | Val | Leu | His | Pro | Glu | 145 | 150 | 155 | 160 |
| Gly | Tyr | Leu | Ile | Thr | Pro | Ala | Trp | Leu | Trp | Glu | Lys | Tyr | Gly | Leu | Arg | 165 | 170 | 175 | |
| Pro | Asp | Gln | Trp | Ala | Asp | Tyr | Arg | Ala | Leu | Thr | Gly | Asp | Glu | Ser | Asp | 180 | 185 | 190 | |
| Asn | Leu | Pro | Gly | Val | Lys | Gly | Ile | Gly | Glu | Lys | Thr | Ala | Arg | Lys | Leu | 195 | 200 | 205 | |
| Leu | Glu | Glu | Trp | Gly | Ser | Leu | Glu | Ala | Leu | Leu | Lys | Asn | Leu | Asp | Arg | 210 | 215 | 220 | |
| Leu | Lys | Pro | Ala | Ile | Arg | Glu | Lys | Ile | Leu | Ala | His | Met | Asp | Asp | Leu | 225 | 230 | 235 | 240 |
| Lys | Leu | Ser | Trp | Asp | Leu | Ala | Lys | Val | Arg | Thr | Asp | Leu | Pro | Leu | Glu | 245 | 250 | 255 | |
| Val | Asp | Phe | Ala | Lys | Arg | Arg | Glu | Pro | Asp | Arg | Glu | Arg | Leu | Arg | Ala | 260 | 265 | 270 | |
| Phe | Leu | Glu | Arg | Leu | Glu | Phe | Gly | Ser | Leu | Leu | His | Glu | Phe | Gly | Leu | 275 | 280 | 285 | |
| Leu | Glu | Ser | Pro | Lys | Ala | Leu | Glu | Glu | Ala | Pro | Trp | Pro | Pro | Pro | Glu | 290 | 295 | 300 | |
| Gly | Ala | Phe | Val | Gly | Phe | Val | Leu | Ser | Arg | Lys | Glu | Pro | Met | Trp | Ala | 305 | 310 | 315 | 320 |
| Asp | Leu | Leu | Ala | Leu | Ala | Ala | Ala | Arg | Gly | Gly | Arg | Val | His | Arg | Ala | 325 | 330 | 335 | |

Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
340 345 350

Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
355 360 365

Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
385 390 395 400

Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
405 410 415

Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
420 425 430

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
435 440 445

Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
450 455 460

Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
515 520 525

Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
580 585 590

Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
625 630 635 640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
660 665 670

Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly
 195 200 205

Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp
 210 215 220

Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala
 225 230 235 240

Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp
 245 250 255

Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala
 260 265 270

Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg
 275 280 285

Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro
 290 295 300

Lys Ser Trp Arg Gly Cys Ile Pro Trp Pro Cys Pro Trp Arg Trp Arg
 305 310 315 320

Trp Gly

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 528 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly
 1 5 10 15

His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr
 20 25 30

Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu
 35 40 45

Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp
 50 55 60

Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala
 65 70 75 80

Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile
 85 90 95

Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val Pro Gly
 100 105 110

Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys Ala Glu Lys
 115 120 125

09941193 082801

Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr Gln
130 135 140

Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr Leu Ile
145 150 155 160

Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp Gln Trp
165 170 175

Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly
180 185 190

Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp
195 200 205

Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala
210 215 220

Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp
225 230 235 240

Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala
245 250 255

Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg
260 265 270

Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro
275 280 285

Lys Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala
290 295 300

Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
305 310 315 320

Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr
325 330 335

Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro
340 345 350

Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
355 360 365

Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
370 375 380

Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
385 390 395 400

Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val
405 410 415

Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg
420 425 430

Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
435 440 445

Val Arg Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
450 455 460

Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His
 465 470 475 480
 Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala
 485 490 495
 Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro
 500 505 510
 Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu
 515 520 525

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 315 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser Gly
 1 5 10 15
 Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly
 20 25 30
 His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr
 35 40 45
 Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu
 50 55 60
 Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp
 65 70 75 80
 Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala
 85 90 95
 Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile
 100 105 110
 Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val Pro Gly
 115 120 125
 Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys Ala Glu Lys
 130 135 140
 Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr Gln
 145 150 155 160
 Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr Leu Ile
 165 170 175
 Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp Gln Trp
 180 185 190
 Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly
 195 200 205

Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp
 210 215 220

Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala
 225 230 235 240

Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp
 245 250 255

Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala
 260 265 270

Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg
 275 280 285

Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro
 290 295 300

Lys Ala Ala Leu Glu His His His His His His
 305 310 315

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

| | |
|---|-----|
| ATGGAGGAGC CGCAGTCAGA TCCTAGCGTC GAGCCCCCTC TGAGTCAGGA AACATTTTCA | 60 |
| GACCTATGGA AACTACTTCC TGAAAACAAC GTTCTGTCCC CCTTGCCGTC CCAAGCAATG | 120 |
| GATGATTTGA TGCTGTCCCC GGACGATATT GAACAATGGT TCACTGAAGA CCCAGGTCCA | 180 |
| GATGAAGCTC CCAGAATGCC AGAGGCTGCT CCCCCGTGG CCCCTGCACC AGCAGCTCCT | 240 |
| ACACCGGCGG CCCCTGCACC AGCCCCCTCC TGGCCCCGTG CATCTTCTGT CCCTTCCCAG | 300 |
| AAAACCTACC AGGGCAGCTA CGGTTTCCGT CTGGGCTTCT TGCATTCTGG GACAGCCAAG | 360 |
| TCTGTGACTT GCACGTACTC CCCTGCCCTC AACAAGATGT TTTGCCAACT GGCCAAGACC | 420 |
| TGCCCTGTGC AGCTGTGGGT TGATTCCACA CCCCCGCCG GCACCCGCGT CCGCGCCATG | 480 |
| GCCATCTACA AGCAGTCACA GCACATGACG GAGGTTGTGA GGCGCTGCCC CCACCATGAG | 540 |
| CGCTGCTCAG ATAGCGATGG TCTGGCCCCT CCTCAGCATC TTATCCGAGT GGAAGGAAAT | 600 |
| TTGCGTGTGG AGTATTTGGA TGACAGAAAC ACTTTTCGAC ATAGTGTGGT GGTGCCCTAT | 660 |
| GAGCCGCTG AGGTTGGCTC TGA CTGTACC ACCATCCACT ACAACTACAT GTGTAACAGT | 720 |
| TCCTGCATGG GCGGCATGAA CCGGAGGCCC ATCCTCACCA TCATCACACT GGAAGACTCC | 780 |
| AGTGGTAATC TACTGGGACG GAACAGCTTT GAGGTGCGTG TTTGTGCCTG TCCTGGGAGA | 840 |
| GACCGGCGCA CAGAGGAAGA GAATCTCCGC AAGAAAGGGG AGCCTCACCA CGAGCTGCCC | 900 |

CCAGGGAGCA CTAAGCGAGC ACTGCCCAAC AACACCAGCT CCTCTCCCCA GCCAAAGAAG 960
 AAACCACTGG ATGGAGAATA TTTCACCCTT CAGATCCGTG GGC GTGAGCG CTTCGAGATG 1020
 TTCCGAGAGC TGAATGAGGC CTTGGAATC AAGGATGCCC AGGCTGGGAA GGAGCCAGGG 1080
 GGGAGCAGGG C TCACTCCAG CCACCTGAAG TCCAAAAAGG GTCAGTCTAC CTCCCGCCAT 1140
 AAAAAACTCA TGTTC AAGAC AGAAGGGCCT GACTCAGACT GA 1182

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATGGAGGAGC CGCAGTCAGA TCCTAGCGTC GAGCCCCCTC TGAGTCAGGA AACATTTTCA 60
 GACCTATGGA AACTACTTCC TGAAAACAAC GTTCTGTCCC CTTGCGCGTC CCAAGCAATG 120
 GATGATTTGA TGCTGTCCCC GGACGATATT GAACAATGGT TCACTGAAGA CCCAGGTCCA 180
 GATGAAGCTC CCAGAATGCC AGAGGCTGCT CCCCCCGTGG CCCCTGCACC AGCAGCTCCT 240
 ACACCGGCGG CCCCTGCACC AGCCCCCTCC TGGCCCCGTGT CATCTTCTGT CCCTTCCCAG 300
 AAAACCTACC AGGGCAGCTA CGGTTTCCGT CTGGGCTTCT TGCATTCTGG GACAGCCAAG 360
 TCTGTGACTT GCACGTACTC CCCTGCCCTC AACAAGATGT TTTGCCAACT GGCCAAGACC 420
 TGCCCTGCGC AGCTGTGGGT TGATTCCACA CCCCCGCCCG GCACCCGCGT CCGCGCCATG 480
 GCCATCTACA AGCAGTCACA GCACATGACG GAGGTTGTGA GGCGCTGCCC CCACCATGAG 540
 CGCTGCTCAG ATAGCGATGG TCTGGCCCCCT CCTCAGCATC TTATCCGAGT GGAAGGAAAT 600
 TTGCGTGTGG AGTATTTGGA TGACAGAAAC ACTTTTCGAC ATAGTGTGGT GGTGCCCTAT 660
 GAGCCGCCTG AGGTTGGCTC TGA CTGTACC ACCATCCACT ACAACTACAT GTGTAACAGT 720
 TCCTGCATGG GCGGCATGAA CCGGAGGCCC ATCCTCACCA TCATCACACT GGAAGACTCC 780
 AGTGGTAATC TACTGGGACG GAACAGCTTT GAGGTGCGTG TTTGTGCCTG TCCTGGGAGA 840
 GACCGGCGCA CAGAGGAAGA GAATCTCCGC AAGAAAGGGG AGCCTCACCA CGAGCTGCCC 900
 CCAGGGAGCA CTAAGCGAGC ACTGCCCAAC AACACCAGCT CCTCTCCCCA GCCAAAGAAG 960
 AAACCACTGG ATGGAGAATA TTTCACCCTT CAGATCCGTG GGC GTGAGCG CTTCGAGATG 1020
 TTCCGAGAGC TGAATGAGGC CTTGGAATC AAGGATGCCC AGGCTGGGAA GGAGCCAGGG 1080
 GGGAGCAGGG C TCACTCCAG CCACCTGAAG TCCAAAAAGG GTCAGTCTAC CTCCCGCCAT 1140
 AAAAAACTCA TGTTC AAGAC AGAAGGGCCT GACTCAGACT GA 1182

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGGAGGAGC CGCAGTCAGA TCCTAGCGTC GAGCCCCCTC TGAGTCAGGA AACATTTTCA 60
GACCTATGGA AACTACTTCC TGAAAACAAC GTTCTGTCCC CCTTGCCGTC CCAAGCAATG 120
GATGATTTGA TGCTGTCCCC GGACGATATT GAACAATGGT TCACTGAAGA CCCAGGTCCA 180
GATGAAGCTC CCAGAATGCC AGAGGCTGCT CCCCCCGTGG CCCCTGCACC AGCAGCTCCT 240
ACACCGGGCG CCCCTGCACC AGCCCCCTCC TGGCCCCCTGT CATCTTCTGT CCCTTCCCAG 300
AAAACCTACC AGGGCAGCTA CGGTTTCCGT CTGGGCTTCT TGCATTCTGG GACAGCCAAG 360
TCTGTGACTT GCACGTACTC CCCTGCCCTC AACAAGATGT TTTGCCAACT GGCCAAGACC 420
TGCCCTGTGC AGCTGTGGGT TGATTCCACA CCCCCGCCCC GCACCCGCGT CCGCGCCATG 480
GCCATCTACA AGCAGTCACA GCACATGACG GAGGTTGTGA GCGCTGCCC CCACCATGAG 540
CGCTGCTCAG ATAGCGATGG TCTGGCCCCCT CCTCAGCATC TTATCCGAGT GGAAGGAAAT 600
TTGCGTGTGG AGTATTTGGA TGACAGAAAC ACTTTTCGAC ATAGTGTGGT GGTGCCCTAT 660
GAGCCGCTG AGGTTGGCTC TGA CTGTG TACC ACCATCCACT ACAACTACAT GTGTAACAGT 720
TCCTGCATGG GCGGCATGAA CCGGAGACCC ATCCTCACCA TCATCACACT GGAAGACTCC 780
AGTGGTAATC TACTGGGACG GAACAGCTTT GAGGTGCGTG TTTGTGCCTG TCCTGGGAGA 840
GACCGGCGCA CAGAGGAAGA GAATCTCCGC AAGAAAGGGG AGCCTCACCA CGAGCTGCCC 900
CCAGGGAGCA CTAAGCGAGC ACTGCCCAAC AACACCAGCT CCTCTCCCCA GCCAAAGAAG 960
AAACCACTGG ATGGAGAATA TTTCACCTT CAGATCCGTG GCGGTGAGCG CTTCGAGATG 1020
TTCCGAGAGC TGAATGAGGC CTTGGAACTC AAGGATGCCC AGGCTGGGAA GGAGCCAGGG 1080
GGGAGCAGGG C TCACTCCAG CCACCTGAAG TCCAAAAAGG GTCAGTCTAC CTCCCGCCAT 1140
AAAAAACTCA TGTTCAAGAC AGAAGGGCCT GACTCAGACT GA 1182

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TCTGGGCTTC TTGCATTCTG

20

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GTTGGGCAGT GCTCGCTTAG

20

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT 60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC 120
ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC 180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC 240
TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA 300
CACTTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC 360
CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGGCC 420
CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT 480
TGAGGTGCGT GTTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG 540
CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA 600
C 601

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

| | |
|--|-----|
| GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT | 60 |
| GCGGAGATTC TCTTCCTCTG TGCGCCGGTC TCTCCCAGGA CAGGCACAAA CACGCACCTC | 120 |
| AAAGCTGTTC CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT | 180 |
| GGGCCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT | 240 |
| GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT | 300 |
| GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCCCTTCC ACTCGGATAA GATGCTGAGG | 360 |
| AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAACCTC | 420 |
| CGTCATGTGC TGTGACTGCT TGTAAGTGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG | 480 |
| TGTGGAATCA ACCCACAGCT GCACAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGTT | 540 |
| GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG | 600 |
| A | 601 |

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 601 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

| | |
|--|-----|
| TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT | 60 |
| CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGCG CAGCTGTGGG TTGATTCCAC | 120 |
| ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC | 180 |
| GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC | 240 |
| TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA | 300 |
| CACTTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCTT GAGGTTGGCT CTGACTGTAC | 360 |
| CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GGCAGCATGA ACCGGAGGCC | 420 |
| CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT | 480 |
| TGAGGTGCGT GTTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG | 540 |
| CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA | 600 |
| C | 601 |

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 601 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT 60
GCGGAGATTG TCTTCCTCTG TGCGCCGGTC TCTCCAGGA CAGGCACAAA CACGCACCTC 120
AAAGCTGTTC CGTCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT 180
GGGCCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT 240
GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT 300
GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCTTCC ACTCGGATAA GATGCTGAGG 360
AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAACCTC 420
CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG 480
TGTGGAATCA ACCCACAGCT GCGCAGGGCA GGTCTTGGCC AGTTGGCAA ACATCTTGTT 540
GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG 600
A 601

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 601 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT 60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC 120
ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC 180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC 240
TCCTCAGCAT CTTATCCGAG TGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA 300
CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC 360
CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGACC 420
CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGTAAT CTACTGGGAC GGAACAGCTT 480
TGAGGTGCGT GTTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG 540
CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA 600

C

601

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

| | |
|---|-----|
| GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT | 60 |
| GCGGAGATTC TCTTCCTCTG TGCGCCGGTC TCTCCAGGA CAGGCACAAA CACGCACCTC | 120 |
| AAAGCTGTTC CGTCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT | 180 |
| GGGTCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT | 240 |
| GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT | 300 |
| GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCTTCC ACTCGGATAA GATGCTGAGG | 360 |
| AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAACCTC | 420 |
| CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG | 480 |
| TGTGGAATCA ACCCAGCT GCACAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGTT | 540 |
| GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG | 600 |
| A | 601 |

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

| | |
|--------------------------|----|
| GAGGATGGGA CTCCGGTTCA TG | 22 |
|--------------------------|----|

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CATGAACCGG AGTCCCATCC TCAC

24

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GCACAAACAT GCACCTCAAA GCT

23

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CAGCTTTGAG GTGCATGTTT GT

22

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

| | |
|---|-----|
| TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT | 60 |
| CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC | 120 |
| ACCCCCGCCG GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC | 180 |
| GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC | 240 |
| TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA | 300 |
| CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC | 360 |
| CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GCGGCATGA ACCGGAGTCC | 420 |
| CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGAAT CTACTGGGAC GGAACAGCTT | 480 |
| TGAGGTGCGT GTTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG | 540 |
| CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA | 600 |

09411974660

C

601

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

| | |
|---|-----|
| GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT | 60 |
| GCGGAGATTC TCTTCCTCTG TGCGCCGGTC TCTCCAGGA CAGGCACAAA CACGCACCTC | 120 |
| AAAGCTGTTC CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT | 180 |
| GGGACTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT | 240 |
| GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT | 300 |
| GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCTTCC ACTCGGATAA GATGCTGAGG | 360 |
| AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAACCTC | 420 |
| CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG | 480 |
| TGTGGAATCA ACCCACAGCT GCACAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGTT | 540 |
| GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG | 600 |
| A | 601 |

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

| | |
|---|-----|
| TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT | 60 |
| CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC | 120 |
| ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC | 180 |
| GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC | 240 |
| TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA | 300 |
| CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC | 360 |
| CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGGCC | 420 |

| | |
|---|-----|
| CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT | 480 |
| TGAGGTGCAT GTTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG | 540 |
| CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA | 600 |
| C | 601 |

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

| | |
|---|-----|
| GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT | 60 |
| GCGGAGATTC TCTTCCTCTG TGCGCCGGTC TCTCCAGGA CAGGCACAAA CATGCACCTC | 120 |
| AAAGCTGTTC CGTCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT | 180 |
| GGGCCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT | 240 |
| GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT | 300 |
| GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCTTCC ACTCGGATAA GATGCTGAGG | 360 |
| AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAACCTC | 420 |
| CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG | 480 |
| TGTGGAATCA ACCCACAGCT GCACAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGTT | 540 |
| GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG | 600 |
| A | 601 |

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 427 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

| | |
|---|-----|
| TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT | 60 |
| CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC | 120 |
| ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC | 180 |
| GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC | 240 |

| | |
|---|-----|
| TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA | 300 |
| CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC | 360 |
| CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GCGGCATGA ACCGGAGTCC | 420 |
| CATCCTC | 427 |

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

| | |
|---|-----|
| CATGAACCGG AGTCCCATCC TCACCATCAT CACACTGGAA GACTCCAGTG GTAATCTACT | 60 |
| GGGACGGAAC AGCTTTGAGG TGCCTGTTTG TGCCTGTCCT GGGAGAGACC GGCGCACAGA | 120 |
| GGAAGAGAAT CTCCGCAAGA AAGGGGAGCC TCACCACGAG CTGCCCCCAG GGAGCACTAA | 180 |
| GCGAGCACTG CCCAAC | 196 |

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

| | |
|---|-----|
| TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT | 60 |
| CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC | 120 |
| ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC | 180 |
| GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC | 240 |
| TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA | 300 |
| CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC | 360 |
| CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GCGGCATGA ACCGGAGGCC | 420 |
| CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT | 480 |
| TGAGGTGCAT GTTTGTGC | 498 |

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CAGCTTTGAG GTGCATGTTT GTGCCTGTCC TGGGAGAGAC CGGCGCACAG AGGAAGAGAA 60
TCTCCGCAAG AAAGGGGAGC CTCACCACGA GCTGCCCCCA GGGAGCACTA AGCGAGCACT 120
GCCCAAC 127

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GGTTTTTCTT TGAGGTTTAG 20

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GCGACACTCC ACCATAGAT 19

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CTGTCTTCAC GCAGAAAGC 19

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GCACGGTCTA CGAGACCTC

19

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GATCTACTAG TCATATGGAT

20

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TCGGTACCCG GGGATCCGAT

20

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

CTGTCTTCAC GCAGAAAGCG TCTGGCCATG GCGTTAGTAT GAGTGTCGTG CAGCCTCCAG

60

GACCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC

120

CAGGACGACC GGGTCCTTTC TTGGATAAAC CCGCTCAATG CCTGGAGATT TGGGCGTGCC

180

CCCGCAAGAC TGCTAGCCGA GTAGTGTGG GTCGCGAAAG GCCTTGTGGT ACTGCCTGAT

240

AGGGTGCCCTG CGAGTGCCCC GGGAGGTCTC GTAGACCGTG C

281

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

| | |
|---|-----|
| CTGTCTTCAC GCAGAAAGCG TCTGGCCATG GCGTTAGTAT GAGTGTCGTG CAGCCTCCAG | 60 |
| GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGACTGTC TTCACGCAGA | 120 |
| AAGCGTCTAG CCATGGCGTT AGTATGAGTG TCGTGCAGCC TCCAGGACCC CCCCTCCCGG | 180 |
| GAGAGCCATA GTGGTCTGCG GAACCGGTGA GTACACCGGA ATTGCCAGGA CGACCGGGTC | 240 |
| CTTTCTTGGA TCAACCCGCT CAATGCCTGG AGATTTGGGC GTGCCCCCGC AAGACTGCTA | 300 |
| GCCGAGTAGT GTTGGGTCGC GAAAGGCCTT GTGGTACTGC CTGATAGGGT GCTTGCGAGT | 360 |
| GCCCCGGGAG GTCTCGTAGA CCGTGC | 386 |

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 281 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

| | |
|---|-----|
| CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCGTG CAGCCTCCAG | 60 |
| GTCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC | 120 |
| CAGGACGACC GGGTCCTTTC TTGGATCAAC CCGCTCAATG CCTGGAGATT TGGGCGTGCC | 180 |
| CCCGCGAGAC TGCTAGCCGA GTAGTGTGG GTGCGGAAAG GCCTTGTGGT ACTGCCTGAT | 240 |
| AGGGTGCTTG CGAGTGCCCC GGGAGGTCTC GTAGACCGTG C | 281 |

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

| | |
|---|-----|
| CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCGTG CAGCCTCCAG | 60 |
| GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC | 120 |
| CAGGACGACC GGGTCCTTTC GTGGATGTAA CCCGCTCAAT GCCTGGAGAT TTGGGCGTGC | 180 |

CCCCGCAAGA CTGCTAGCCG AGTAGTGTG GGTGCGGAAA GGCCTTGTGG TACTGCCTGA 240
TAGGGTGCTT GCGAGTGCCC CGGGAGGTCT CGTAGACCGT GC 282

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCGTA CAGCCTCCAG 60
GCCCCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC 120
CGGGAAGACT GGGTCCTTTC TTGGATAAAC CCACTCTATG CCCGGCCATT TGGGCGTGCC 180
CCCGCAAGAC TGCTAGCCGA GTAGCGTTGG GTTGCGAAAG GCCTTGTGGT ACTGCCTGAT 240
AGGGTGCTTG CGAGTACCCC GGGAGGTCTC GTAGACCGTG C 281

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CTGTCTTCAC GCAGAAAGCG CCTAGCCATG GCGTTAGTAC GAGTGTCGTG CAGCCTCCAG 60
GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC 120
TGGGGTGACC GGGTCCTTTC TTGGAGCAAC CCGCTCAATA CCCAGAAATT TGGGCGTGCC 180
CCCGCGAGAT CACTAGCCGA GTAGTGTGG GTGCGGAAAG GCCTTGTGGT ACTGCCTGAT 240
AGGGTGCTTG CGAGTGCCCC GGGAGGTCTC GTAGACCGTG C 281

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAGGCACCC TATCAGGCAG TACCACAAGG 60

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| CCTTTTCGCGA | CCCAACACTA | CTCGGCTAGC | AGTCTTGCGG | GGGCACGCCC | AAATCTCCAG | 120 |
| GCATTGAGCG | GGTTTATCCA | AGAAAGGACC | CGGTCGTCCT | GGCAATTCCG | GTGTACTCAC | 180 |
| CGGTTCCGCA | GACCACTATG | GCTCTCCCGG | GAGGGGGGGT | CCTGGAGGCT | GCACGACACT | 240 |
| CATACTAACG | CCATGGCCAG | ACGCTTTCTG | CGTGAAGACA | G | | 281 |

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| GCACGGTCTA | CGAGACCTCC | CGGGGCACTC | GCAAGCACCC | TATCAGGCAG | TACCACAAGG | 60 |
| CCTTTTCGCGA | CCCAACACTA | CTCGGCTAGC | AGTCTTGCGG | GGGCACGCCC | AAATCTCCAG | 120 |
| GCATTGAGCG | GGTTGATCCA | AGAAAGGACC | CGGTCGTCCT | GGCAATTCCG | GTGTACTCAC | 180 |
| CGGTTCCGCA | GACCACTATG | GCTCTCCCGG | GAGGGGGGGT | CCTGGAGGCT | GCACGACACT | 240 |
| CATACTAACG | CCATGGCTAG | ACGCTTTCTG | CGTGAAGACA | G | | 281 |

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| GCACGGTCTA | CGAGACCTCC | CGGGGCACTC | GCAAGCACCC | TATCAGGCAG | TACCACAAGG | 60 |
| CCTTTTCGCGA | CCCAACACTA | CTCGGCTAGC | AGTCTCGCGG | GGGCACGCCC | AAATCTCCAG | 120 |
| GCATTGAGCG | GGTTGATCCA | AGAAAGGACC | CGGTCGTCCT | GGCAATTCCG | GTGTACTCAC | 180 |
| CGGTTCCGCA | GACCACTATG | GCTCTCCCGG | GAGGGGGGGA | CCTGGAGGCT | GCACGACACT | 240 |
| CATACTAACG | CCATGGCTAG | ACGCTTTCTG | CGTGAAGACA | G | | 281 |

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG 60
CCTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTTGCGG GGGCACGCCC AAATCTCCAG 120
GCATTGAGCG GGTACATCC ACGAAAGGAC CCGGTCGTCC TGGCAATTCC GGTGTACTCA 180
CCGGTCCGCG AGACCACTAT GGCTCTCCCG GGAGGGGGGG TCCTGGAGGC TGCACGACAC 240
TCATACTAAC GCCATGGCTA GACGCTTTCT GCGTGAAGAC AG 282

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCACGGTCTA CGAGACCTCC CGGGGTACTC GCAAGCACCC TATCAGGCAG TACCACAAGG 60
CCTTTCGCAA CCCAACGCTA CTCGGCTAGC AGTCTTGCGG GGGCACGCCC AAATGGCCGG 120
GCATAGAGTG GGTATTATCCA AGAAAGGACC CAGTCTTCCC GGCAATTCCG GTGTACTCAC 180
CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGG CCTGGAGGCT GTACGACACT 240
CATACTAACG CCATGGCTAG ACGCTTTCTG CGTGAAGACA G 281

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG 60
CCTTTCGCGA CCCAACACTA CTCGGCTAGT GATCTCGCGG GGGCACGCCC AAATTTCTGG 120
GTATTGAGCG GGTGCTCCA AGAAAGGACC CGGTCACCCC AGCGATTCCG GTGTACTCAC 180
CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGT CCTGGAGGCT GCACGACACT 240
CGTACTAACG CCATGGCTAG GCGCTTTCTG CGTGAAGACA G 281

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

ATCAACATCC GGCCGGTGGT

20

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GGGGCCTCGC TACGGACCAG

20

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ATCAACATCC GGCCGGTGGT CGCCGCGATC AAGGAGTTCT TCGGCACCAG CCAGCTGAGC 60
CAATTCATGG ACCAGAACAA CCCGCTGTCTG GGGTTGACCC ACAAGCGCCG ACTGTCGGCG 120
CTGGGGCCCG GCGGTCTGTC ACGTGAGCGT GCCGGGCTGG AGGTCCGCGA CGTGCACCCG 180
TCGCACTACG GCCGGATGTG CCCGATCGAA ACCCCTGAGG GGCCCAACAT CGGTCTGATC 240
GGCTCGCTGT CGGTGTACGC GCGGGTCAAC CCGTTCGGGT TCATCGAAAC GCCGTACCGC 300
AAGGTGGTCG ACGGCGTGGT TAGCGACGAG ATCGTGTACC TGACCGCCGA CGAGGAGGAC 360
CGCCACGTGG TGGCACAGGC CAATTCGCCG ATCGATGCGG ACGGTCGCTT CGTCGAGCCG 420
CGCGTGCTGG TCCGCCGCAA GCGGGGCGAG GTGGAGTACG TGCCCTCGTC TGAGGTGGAC 480
TACATGGACG TCTCGCCCCG CCAGATGGTG TCGGTGGCCA CCGCGATGAT TCCCTTCCTG 540
GAGCACGACG ACGCCAACCG TGCCCTCATG GGGGCAAACA TGCAGCGCCA GGCGGTGCCG 600
CTGGTCCGTA GCGAGGCCCC 620

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

| | | | | | | |
|-------------|------------|-------------|------------|------------|------------|-----|
| ATCAACATCC | GGCCGGTGGT | CGCCGCGATC | AAGGAGTTCT | TCGGCACCAG | CCAGCTGAGC | 60 |
| CAATTCATGG | ACCAGAACAA | CCCGCTGTCTG | GGGTTGACCT | ACAAGCGCCG | ACTGTCGGCG | 120 |
| CTGGGGCCCCG | GCGGTCTGTC | ACGTGAGCGT | GCCGGGCTGG | AGGTCCGCGA | CGTGCACCCG | 180 |
| TCGCACTACG | GCCGGATGTG | CCCGATCGAA | ACCCCTGAGG | GGCCCAACAT | CGGTCTGATC | 240 |
| GGCTCGCTGT | CGGTGTACGC | GCGGGTCAAC | CCGTTCCGGT | TCATCGAAAC | GCCGTACCGC | 300 |
| AAGGTGGTCG | ACGGCGTGGT | TAGCGACGAG | ATCGTGTACC | TGACCGCCGA | CGAGGAGGAC | 360 |
| CGCCACGTGG | TGGCACAGGC | CAATTCGCCG | ATCGATGCGG | ACGGTCGCTT | CGTCGAGCCG | 420 |
| CGCGTGCTGG | TCCGCCGCAA | GGCGGGCGAG | GTGGAGTACG | TGCCCTCGTC | TGAGGTGGAC | 480 |
| TACATGGACG | TCTCGCCCCG | CCAGATGGTG | TCGGTGGCCA | CCGCGATGAT | TCCCTTCCTG | 540 |
| GAGCACGACG | ACGCCAACCG | TGCCCTCATG | GGGGCAAACA | TGCAGCGCCA | GGCGGTGCCG | 600 |
| CTGGTCCGTA | GCGAGGCCCC | | | | | 620 |

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

| | | | | | | |
|-------------|------------|-------------|------------|------------|------------|-----|
| ATCAACATCC | GGCCGGTGGT | CGCCGCGATC | AAGGAGTTCT | TCGGCACCAG | CCAGCTGAGC | 60 |
| CAATTCATGG | ACCAGAACAA | CCCGCTGTCTG | GGGTTGACCC | ACAAGCGCCG | ACTGTTGGCG | 120 |
| CTGGGGCCCCG | GCGGTCTGTC | ACGTGAGCGT | GCCGGGCTGG | AGGTCCGCGA | CGTGCACCCG | 180 |
| TCGCACTACG | GCCGGATGTG | CCCGATCGAA | ACCCCTGAGG | GGCCCAACAT | CGGTCTGATC | 240 |
| GGCTCGCTGT | CGGTGTACGC | GCGGGTCAAC | CCGTTCCGGT | TCATCGAAAC | GCCGTACCGC | 300 |
| AAGGTGGTCG | ACGGCGTGGT | TAGCGACGAG | ATCGTGTACC | TGACCGCCGA | CGAGGAGGAC | 360 |
| CGCCACGTGG | TGGCACAGGC | CAATTCGCCG | ATCGATGCGG | ACGGTCGCTT | CGTCGAGCCG | 420 |
| CGCGTGCTGG | TCCGCCGCAA | GGCGGGCGAG | GTGGAGTACG | TGCCCTCGTC | TGAGGTGGAC | 480 |
| TACATGGACG | TCTCGCCCCG | CCAGATGGTG | TCGGTGGCCA | CCGCGATGAT | TCCCTTCCTG | 540 |
| GAGCACGACG | ACGCCAACCG | TGCCCTCATG | GGGGCAAACA | TGCAGCGCCA | GGCGGTGCCG | 600 |
| CTGGTCCGTA | GCGAGGCCCC | | | | | 620 |

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 620 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

| | |
|--|-----|
| GGGGCCTCGC TACGGACCAG CGGCACCGCC TGGCGCTGCA TGTTTGCCCC CATGAGGGCA | 60 |
| CGGTTGGCGT CGTCGTGCTC CAGGAAGGGA ATCATCGCGG TGGCCACCGA CACCATCTGG | 120 |
| CGGGGCGAGA CGTCCATGTA GTCCACCTCA GACGAGGGCA CGTACTCCAC CTCGCCCCGCC | 180 |
| TTGCGGCGGA CCAGCACGCG CGGCTCGACG AAGCGACCGT CCGCATCGAT CGGCGAATTG | 240 |
| GCCTGTGCCA CCACGTGGCG GTCCTCCTCG TCGGCGGTCA GGTACACGAT CTCGTGCTA | 300 |
| ACCACGCCGT CGACCACCTT GCGGTACGGC GTTTCGATGA ACCCGAACGG GTTGACCCGC | 360 |
| GCGTACACCG ACAGCGAGCC GATCAGACCG ATGTTGGGCC CCTCAGGGGT TTCGATCGGG | 420 |
| CACATCCGGC CGTAGTGCGA CGGGTGCACG TCGCGGACCT CCAGCCCGGC ACGCTCACGT | 480 |
| GACAGACCGC CGGGCCCCAG CGCCGACAGT CGGCGCTTGT GGGTCAACCC CGACAGCGGG | 540 |
| TTGTTCTGGT CCATGAATTG GCTCAGCTGG CTGGTGCCGA AGAACTCCTT GATCGCGGCG | 600 |
| ACCACCGGCC GGATGTTGAT | 620 |

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 620 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

| | |
|--|-----|
| GGGGCCTCGC TACGGACCAG CGGCACCGCC TGGCGCTGCA TGTTTGCCCC CATGAGGGCA | 60 |
| CGGTTGGCGT CGTCGTGCTC CAGGAAGGGA ATCATCGCGG TGGCCACCGA CACCATCTGG | 120 |
| CGGGGCGAGA CGTCCATGTA GTCCACCTCA GACGAGGGCA CGTACTCCAC CTCGCCCCGCC | 180 |
| TTGCGGCGGA CCAGCACGCG CGGCTCGACG AAGCGACCGT CCGCATCGAT CGGCGAATTG | 240 |
| GCCTGTGCCA CCACGTGGCG GTCCTCCTCG TCGGCGGTCA GGTACACGAT CTCGTGCTA | 300 |
| ACCACGCCGT CGACCACCTT GCGGTACGGC GTTTCGATGA ACCCGAACGG GTTGACCCGC | 360 |
| GCGTACACCG ACAGCGAGCC GATCAGACCG ATGTTGGGCC CCTCAGGGGT TTCGATCGGG | 420 |
| CACATCCGGC CGTAGTGCGA CGGGTGCACG TCGCGGACCT CCAGCCCGGC ACGCTCACGT | 480 |

| | |
|---|-----|
| GACAGACCGC CGGGCCCCAG CGCCGACAGT CGGCGCTTGT AGGTCAACCC CGACAGCGGG | 540 |
| TTGTTCTGGT CCATGAATTG GCTCAGCTGG CTGGTGCCGA AGAACTCCTT GATCGCGGCG | 600 |
| ACCACCGGCC GGATGTTGAT | 620 |

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

| | |
|--|-----|
| GGGGCCTCGC TACGGACCAG CGGCACCGCC TGGCGCTGCA TGTTCGCCCC CATGAGGGCA | 60 |
| CGGTTGGCGT CGTCGTGCTC CAGGAAGGGA ATCATCGCGG TGGCCACCGA CACCATCTGG | 120 |
| CGGGGCGAGA CGTCCATGTA GTCCACCTCA GACGAGGGCA CGTACTCCAC CTCGCCCCGCC | 180 |
| TTGCGGCGGA CCAGCACGCG CGGCTCGACG AAGCGACCGT CCGCATCGAT CGGCGAATTG | 240 |
| GCCTGTGCCA CCACGTGGCG GTCCTCCTCG TCGGCGGTCA GGTACACGAT CTCGTCGCTA | 300 |
| ACCACGCCGT CGACCACCTT GCGGTACGGC GTTTCGATGA ACCCGAACGG GTTGACCCGC | 360 |
| GCGTACACCG ACAGCGAGCC GATCAGACCG ATGTTGGGCC CCTCAGGGGT TTCGATCGGG | 420 |
| CACATCCGGC CGTAGTGCGA CGGGTGACG TCGCGGACCT CCAGCCCGGC ACGCTCACGT | 480 |
| GACAGACCGC CGGGCCCCAG CGCCAACAGT CGGCGCTTGT GGGTCAACCC CGACAGCGGG | 540 |
| TTGTTCTGGT CCATGAATTG GCTCAGCTGG CTGGTGCCGA AGAACTCCTT GATCGCGGCG | 600 |
| ACCACCGGCC GGATGTTGAT | 620 |

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

| | |
|-----------------------|----|
| AGCTCGTATG GCACCGGAAC | 20 |
|-----------------------|----|

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TTGACCTCCC ACCCGACTTG

20

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 620 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA GCGGCATCGA GGTCGTATGG 60
ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG 120
GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC 180
GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC 240
CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC 300
GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT 360
CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG 420
GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG 480
ATCCGGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGGC GGCGGCGTCG 540
TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA 600
CAAGTCGGGT GGGAGGTCAA 620

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 620 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA CCGGCATCGA GGTCGTATGG 60
ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG 120
GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC 180
GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC 240
CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC 300

| | |
|---|-----|
| GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT | 360 |
| CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG | 420 |
| GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG | 480 |
| ATCCGGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGGC GGC GGCGCTCG | 540 |
| TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA | 600 |
| CAAGTCGGGT GGGAGGTCAA | 620 |

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 620 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

| | |
|--|-----|
| AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA GCGGCATCGA GGTCGTATGG | 60 |
| ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG | 120 |
| GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC | 180 |
| GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC | 240 |
| CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC | 300 |
| GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT | 360 |
| CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG | 420 |
| GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG | 480 |
| ATCTGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGGC GGC GGCGCTCG | 540 |
| TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA | 600 |
| CAAGTCGGGT GGGAGGTCAA | 620 |

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 620 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

| | |
|---|-----|
| AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA CCGGCATCGA GGTCGTATGG | 60 |
| ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG | 120 |

| | |
|---|-----|
| GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC | 180 |
| GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC | 240 |
| CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC | 300 |
| GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT | 360 |
| CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG | 420 |
| GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG | 480 |
| ATCCTGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGGC GGCGGCGTCG | 540 |
| TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA | 600 |
| CAAGTCGGGT GGGAGGTCAA | 620 |

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

| | |
|---|-----|
| TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC | 60 |
| TTGTCGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA | 120 |
| GTCAATCCCG ATGCCCGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG | 180 |
| TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC | 240 |
| CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCCTTGGCG | 300 |
| AACTCGTCGG CCAATTCTCT GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC | 360 |
| GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG | 420 |
| AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA | 480 |
| GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC | 540 |
| CATTCGTCG GGGTGTTCGT CCATACGACC TCGATGCCGC TGGTGATCGC GTCCTTACCG | 600 |
| GTTCCGGTGC CATACGAGCT | 620 |

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

| | |
|---|-----|
| TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC | 60 |
| TTGTCGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA | 120 |
| GTCAATCCCG ATGCCCGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG | 180 |
| TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC | 240 |
| CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCCTTGGCG | 300 |
| AACTCGTCGG CCAATTCCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC | 360 |
| GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG | 420 |
| AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA | 480 |
| GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC | 540 |
| CATTCGTCG GGGTGTTCGT CCATACGACC TCGATGCCGG TGGTGATCGC GTCCTTACCG | 600 |
| GTTCCGGTGC CATACGAGCT | 620 |

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

| | |
|---|-----|
| TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC | 60 |
| TTGTCGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA | 120 |
| GTCAATCCCG ATGCCCGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG | 180 |
| TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC | 240 |
| CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCCTTGGCG | 300 |
| AACTCGTCGG CCAATTCCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC | 360 |
| GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG | 420 |
| AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA | 480 |
| GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC | 540 |
| CATTCGTCG GGGTGTTCGT CCATACGACC TCGATGCCGC TGGTGATCGC GTCCTTACCG | 600 |
| GTTCCGGTGC CATACGAGCT | 620 |

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

| | |
|--|-----|
| TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC | 60 |
| TTGTGCGTAC CACGGAAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA | 120 |
| GTCAATCCCG ATGCCAGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG | 180 |
| TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC | 240 |
| CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCCTTGGCG | 300 |
| AACTCGTCGG CCAATTCTCT GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC | 360 |
| GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCCCGG | 420 |
| AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA | 480 |
| GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC | 540 |
| CATTTGTCG GGGTGTTCGT CCATACGACC TCGATGCCGG TGGTGATCGC GTCCTTACCG | 600 |
| GTTCCGGTGC CATAAGAGCT | 620 |

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

| | |
|-----------------------|----|
| AGAGTTTGAT CCTGGCTCAG | 20 |
|-----------------------|----|

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

| | |
|--------------------|----|
| GGCGGACGGG TGAGTAA | 17 |
|--------------------|----|

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CTGCTGCCTC CCGTAGGAGT

20

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ATGACGTCAA GTCATCATGG CCCTTACGA

29

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GTACAAGGCC CGGGAACGTA TTCACCG

27

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GCAACGAGCG CAACCC

16

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ATGACGTCAA GTCATCATGG CCCTTA

26

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

AAATTGAAGA GTTTGATCAT GGCTCAGATT GAACGCTGGC GGCAGGCCTA ACACATGCAA 60
GTCGAACGGT AACAGGAAGA AGCTTGCTTC TTTGCTGACG AGTGGCGGAC GGGTGAGTAA 120
TGTCTGGGAA ACTGCCTGAT GGAGGGGGAT AACTACTGGA AACGGTAGCT AATACCGCAT 180
AACGTCGCAA GACCAAAGAG GGGGACCTTC GGGCCTCTTG CCATCGGATG TGCCCAGATG 240
GGATTAGCTA GTAGGTGGGG TAACGGCTCA CCTAGGCGAC GATCCCTAGC TGGTCTGAGA 300
GGATGACCAG CCACACTGGA ACTGAGACAC GGTCCAGACT CCTACGGGAG GCAGCAGTGG 360
GGAATATTGC ACAATGGGCG CAAGCCTGAT GCAGCCATGC CGCGTGTATG AAGAAGGCCT 420
TCGGGTTGTA AAGTACTTTC AGCGGGGAGG AAGGGAGTAA AGTTAATACC TTTGCTCATT 480
GACGTTACCC GCAGAAGAAG CACCGGCTAA CTCCGTGCCA GCAGCCGCGG TAATACGGAG 540
GGTGCAAGCG TTAATCGGAA TTAATGGGCG TAAAGCGCAC GCAGGCGGTT TGTTAAGTCA 600
GATGTGAAAT CCCCGGGCTC AACCTGGGAA CTGCATCTGA TACTGGCAAG CTTGAGTCTC 660
GTAGAGGGGG GTAGAATTCC AGGTGTAGCG GTGAAATGCG TAGAGATCTG GAGGAATACC 720
GGTGGCGAAG GCGGCCCCCT GGACGAAGAC TGACGCTCAG GTGCGAAAGC GTGGGGAGCA 780
AACAGGATTA GATACCCTGG TAGTCCACGC CGTAAACGAT GTCGACTTGG AGGTTGTGCC 840
CTTGAGGCGT GGCTTCCGGA GCTAACGCGT TAAGTCGACC GCCTGGGGAG TACGGCCGCA 900
AGGTTAAAAC TCAAATGAAT TGACGGGGGC CCGCACAAGC GGTGGAGCAT GTGGTTTAAT 960
TCGATGCAAC GCGAAGAACC TTACCTGGTC TTGACATCCA CGGAAGTTTT CAGAGATGAG 1020
AATGTGCCTT CGGGAACCGT GAGACAGGTG CTGCATGGCT GTCGTCAGCT CGTGTTGTGA 1080
AATGTTGGGT TAAGTCCCGC AACGAGCGCA ACCCTTATCC TTTGTTGCCA GCGGTCCGGC 1140
CGGGA ACTCA AAGGAGACTG CCAGTGATAA ACTGGAGGAA GGTGGGGATG ACGTCAAGTC 1200
ATCATGGCCC TTACGACCAG GGCTACACAC GTGCTACAAT GGCGCATAA AAGAGAAGCG 1260
ACCTCGCGAG AGCAAGCGGA CCTCATAAAG TGCGTCGTAG TCCGATTGG AGTCTGCAAC 1320
TCGACTCCAT GAAGTCGGAA TCGCTAGTAA TCGTGGATCA GAATGCCACG GTGAATACGT 1380

| | | |
|--|------------|------|
| TCCCGGGCCT TGTACACACC GCCCGTCACA CCATGGGAGT GGGTTGCAA | AGAAGTAGGT | 1440 |
| AGCTTAACCT TCGGGAGGGC GCTTACCACT TTGTGATTCA TGACTGGGGT | GAAGTCGTAA | 1500 |
| CAAGGTAACC GTAGGGGAAC CTGCGGTTGG ATCACCTCCT TA | | 1542 |

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

09941193 091650
T08280 "E5T4650"

| | |
|--|------|
| TTTTTATGGA GAGTTTGATC CTGGCTCAGA GTGAACGCTG GCGGCGTGCC TAATACATGC | 60 |
| AAGTCGAACG ATGAAGCTTC TAGCTTGCTA GAAGTGGATT AGTGGCGCAC GGGTGAGTAA | 120 |
| GGTATAGTTA ATCTGCCCTA CACAAGAGGA CAACAGTTGG AAACGACTGC TAATACTCTA | 180 |
| TACTCCTGCT TAACACAAGT TGAGTAGGGA AAGTTTTTCG GTGTAGGATG AGACTATATA | 240 |
| GTATCAGCTA GTTGGTAAGG TAATGGCTTA CCAAGGCTAT GACGCTTAAC TGGTCTGAGA | 300 |
| GGATGATCAG TCACACTGGA ACTGAGACAC GGTCCAGACT CCTACGGGAG GCAGCAGTAG | 360 |
| GGAATATTGC GCAATGGGGG AAACCCTGAC GCAGCAACGC CGCGTGGAGG ATGACACTTT | 420 |
| TCGGAGCGTA AACTCCTTTT CTTAGGGAAG AATTCTGACG GTACCTAAGG AATAAGCACC | 480 |
| GGCTAACTCC GTGCCAGCAG CCGCGGTAAT ACGGAGGGTG CAAGCGTTAC TCGGAATCAC | 540 |
| TGGGCGTAAA GGGCGCGTAG GCGGATTATC AAGTCTCTTG TGAAATCTAA TGGCTTAACC | 600 |
| ATTAACTGC TTGGGAACT GATAGTCTAG AGTGAGGGAG AGGCAGATGG AATTGGTGGT | 660 |
| GTAGGGGTAA AATCCGTAGA TATCACCAAG AATACCCATT GCGAAGGCGA TCTGCTGGAA | 720 |
| CTCAACTGAC GCTAAGGCGC GAAAGCGTGG GGAGCAAACA GGATTAGATA CCCTGGTAGT | 780 |
| CCACGCCCTA AACGATGTAC ACTAGTTGTT GGGGTGCTAG TCATCTCAGT AATGCAGCTA | 840 |
| ACGCATTAAG TGTACCGCCT GGGGAGTACG GTCGCAAGAT TAAAACTCAA AGGAATAGAC | 900 |
| GGGGACCCGC ACAAGCGGTG GAGCATGTGG TTTAATTCTGA AGATACGCGA AGAACCTTAC | 960 |
| CTGGGCTTGA TATCCTAAGA ACCTTTTAGA GATAAGAGGG TGCTAGCTTG CTAGAACTTA | 1020 |
| GAGACAGGTG CTGCACGGCT GTCGTCAGCT CGTGTCGTGA GATGTTGGGT TAAGTCCCGC | 1080 |
| AACGAGCGCA ACCCACGTAT TTAGTTGCTA ACGGTTCCGC CGAGCACTCT AAATAGACTG | 1140 |
| CCTTCGTAAG GAGGAGGAAG GTGTGGACGA CGTCAAGTCA TCATGGCCCT TATGCCCAGG | 1200 |
| GCGACACACG TGCTACAATG GCATATAGAA TGAGACGCAA TACCGCGAGG TGGAGCAAAT | 1260 |
| CTATAAAATA TGTCCCAGTT CGGATTGTTC TCTGCAACTC GAGAGCATGA AGCCGGAATC | 1320 |

| | |
|--|------|
| GCTAGTAATC GTAGATCAGC CATGCTACGG TGAATACGTT CCCGGGTCTT GTACTCACCG | 1380 |
| CCCGTCACAC CATGGGAGTT GATTTCACCTC GAAGCCGGAA TACTAAACTA GTTACCGTCC | 1440 |
| ACAGTGGAAAT CAGCGACTGG GGTGAAGTCG TAACAAGGTA ACCGTAGGAG AACCTGCGGT | 1500 |
| TGGATCACCT CCT | 1513 |

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1555 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

| | |
|---|------|
| TTTTATGGAG AGTTTGATCC TGGCTCAGGA TGAACGCTGG CGGCGTGCCT AATACATGCA | 60 |
| AGTCGAGCGA ACGGACGAGA AGCTTGCTTC TCTGATGTTA GCGGCGGACG GGTGAGTAAC | 120 |
| ACGTGGATAA CCTACCTATA AGACTGGGAT AACTTCGGGA AACCGGAGCT AATACCGGAT | 180 |
| AATATTTTGA ACCGCATGGT TCAAAAGTGA AAGACGGTCT TGCTGTCACT TATAGATGGA | 240 |
| TCCGCGCTGC ATTAGCTAGT TGGTAAGGTA ACGGCTTACC AAGGCAACGA TACGTAGCCG | 300 |
| ACCTGAGAGG GTGATCGGCC AACTTGAAC TGAGACACGG TCCAGACTCC TACGGGAGGC | 360 |
| AGCAGTAGGG AATCTTCCGC AATGGGCGAA AGCCTGACGG AGCAACGCCG CGTGAGTGAT | 420 |
| GAAGGTCTTC GGATCGTAAA ACTCTGTTAT TAGGGAAGAA CATATGTGTA AGTAACTGTG | 480 |
| CACATCTTGA CGGTACCTAA TCAGAAAGCC ACGGCTAACT ACGTGCCAGC AGCCGCGGTA | 540 |
| ATACGTAGGT GGCAAGCGTT ATCCGGAATT ATTGGGCGTA AAGCGCGCGT AGGCGGTTTT | 600 |
| TTAAGTCTGA TGTGAAAGCC CACGGCTCAA CCGTGGAGGG TCATTGGAAA CTGGAAAAC | 660 |
| TGAGTGCAGA AGAGGAAAGT GGAATTCCAT GTGTAGCGGT GAAATGCGCA GAGATATGGA | 720 |
| GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAACTG ACGCTGATGT GCGAAAGCGT | 780 |
| GGGGATCAAA CAGGATTAGA TACCCTGGTA GTCCACGCCG TAAACGATGA GTGCTAAGTG | 840 |
| TTAGGGGGTT TCCGCCCTT AGTGCTGCAG CTAACGCATT AAGCACTCCG CCTGGGGAGT | 900 |
| ACGACCGCAA GGTTGAAACT CAAAGGAATT GACGGGGACC CGCACAAGCG GTGGAGCATG | 960 |
| TGGTTTAATT CGAAGCAACG CGAAGAACCT TACCAAATCT TGACATCCTT TGACAACTCT | 1020 |
| AGAGATAGAG CCTTCCCCTT CGGGGGACAA AGTGACAGGT GGTGCATGGT TGTCGTCAGC | 1080 |
| TCGTGTCGTG AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCCCTAAG CTTAGTTGCC | 1140 |
| ATCATTAAGT TGGGCACTCT AAGTTGACTG CCGGTGACAA ACCGGAGGAA GGTGGGGATG | 1200 |
| ACGTCAAATC ATCATGCCCC TTATGATTTG GGCTACACAC GTGCTACAAT GGACAATACA | 1260 |

SECRET